GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 31, 2005, 13:48:48 ; Search time 174 Seconds
(without alignments)
831.313 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 1970
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1970	100.0	374	2	AAR79165	Aar79165 Human mon
2	1970	100.0	374	4	AAG80107	Aag80107 Human CCR
3	1970	100.0	374	6	ABU09083	Abu09083 Human che
4	1970	100.0	374	7	ADD44861	Add44861 Human Pro
5	1970	100.0	374	7	ADD44865	Add44865 Human Pro
6	1970	100.0	374	7	ADP65146	Adp65146 Human che
7	1970	100.0	374	8	ADO29221	Ado29221 Human GPC
8	1970	100.0	374	8	ADQ67847	Adq67847 Human che
9	1823	92.5	344	5	ABG92881	Abg92881 Class I r

10	1823	92.5	344	6	ABU61655	Abu61655 Human mon
11	1823	92.5	344	7	ADF72129	Adf72129 Human G-p
12	1823	92.5	344	8	ADP86217	Adp86217 Human MCP
13	1727.5	87.7	329	4	AAB46859	Aab46859 Human MCP
14	1727.5	87.7	329	5	ABB81055	Abb81055 Human MCP
15	1727.5	87.7	329	8	ADR16266	Adr16266 Human MCP
16	1651.5	83.8	360	2	AAR79166	Aar79166 Human mon
17	1651.5	83.8	360	2	AAW35833	Aaw35833 Human mon
18	1651.5	83.8	360	4	AAG80108	Aag80108 Human CCR
19	1651.5	83.8	360	4	AAU07614	Aau07614 Human wil
20	1651.5	83.8	360	6	ABP97725	Abp97725 Amino aci
21	1651.5	83.8	360	6	ABP81987	Abp81987 Human C-C
22	1651.5	83.8	360	8	ADM67225	Adm67225 Human adi
23	1651.5	83.8	360	8	ADL82831	Adl82831 Human PRO
24	1650.5	83.8	360	4	AAU07613	Aau07613 Human CCR
25	1645.5	83.5	360	4	ABB56340	Abb56340 Non-endog
26	1589.5	80.7	347	7	ADF56627	Adf56627 Partial h
27	1332.5	67.6	373	8	ADM67224	Adm67224 Murine ad
28	1332.5	67.6	373	8	ADO29222	Ado29222 Mouse GPC
29	1332.5	67.6	373	8	ADP74040	Adp74040 Murine CC
30	1244	63.1	354	8	ADO29228	Ado29228 Mouse GPC
31	1236	62.7	352	4	AAG79089	Aag79089 Amino aci
32	1234	62.6	354	2	AAW54037	Aaw54037 Mouse CC-
33	1230	62.4	354	7	ADD44859	Add44859 Rat Prote
34	1230	62.4	354	7	ADD44863	Add44863 Rat Prote
35	1224	62.1	352	2	AAW27407	Aaw27407 Human CCR
36	1224	62.1	352	2	AAW27123	Aaw27123 Human che
37	1224	62.1	352	2	AAW27125	Aaw27125 Macaque c
38	1224	62.1	352	2	AAW23835	Aaw23835 Human CC
39	1224	62.1	352	2	AAW88232	Aaw88232 HIV-1 co-
40	1224	62.1	352	4	AAE07048	Aae07048 Human G-p
41	1224	62.1	352	4	AAG80111	Aag80111 Human CCR
42	1224	62.1	352	4	AAE04321	Aae04321 Human che
43	1224	62.1	352	4	AAE07039	Aae07039 Human G-p
44	1224	62.1	352	4	AAB46858	Aab46858 Human HDG
45	1224	62.1	352	4	AAB83354	Aab83354 Human CCR

ALIGNMENTS

RESULT 1
AAR79165
ID AAR79165 standard; protein; 374 AA.
XX
AC AAR79165;
XX
DT 25-MAR-2003 (revised)
DT 29-DEC-1995 (first entry)
XX
DE Human monocyte chemoattractant protein-1 receptor MCP-1RA.
XX
KW Monocyte chemoattractant protein-1 receptor; MCR-1R; chemokine.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers

FT Domain 1. .48
FT /label= extracellular
FT Domain 49. .70
FT /label= transmembrane
FT Domain 80. .700
FT /label= transmembrane
FT Domain 115. .136
FT /label= transmembrane
FT Domain 154. .178
FT /label= transmembrane
FT Domain 204. .231
FT /label= transmembrane
FT Domain 244. .268
FT /label= transmembrane
FT Domain 295. .313
FT /label= transmembrane
FT Region 314. .375
FT /label= carboxyl tail
XX
PN WO9519436-A1.
XX
PD 20-JUL-1995.
XX
PF 11-JAN-1995; 95WO-US000476.
XX
PR 13-JAN-1994; 94US-00182962.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Charo I, Coughlin S;
XX
DR WPI; 1995-263866/34.
DR N-PSDB; AAQ96297.
XX
PT DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
PT for identifying antagonists and for treating diseases characterised by
PT monocytic infiltrates.
XX
PS Claim 2; Fig 1; 84pp; English.
XX
CC To identify and clone new members of the chemokine receptor gene family,
CC degenerate oligo primers were designed corresp. to the conserved
CC sequences R79167 in the second and R79168 in the third transmembrane
CC domains of the MIP-1alpha/RANTES receptor, the IL-8 receptors and the
CC HUMSTRS orphan receptor (GenBank Accession #M99293. The degenerate oligo
CC incorporating EcoRI and XhoI sites at their 5' ends are Q96299 and
CC Q96300. Amplification of cDNA derived from MM6 cells with the primers
CC yieled a number of PCR products. One cDNA appeared to encode a novel
CC protein. To obtain a full-length version of this clone, a MM6 cDNA
CC library was constructed in pFROG and probed with the PCR product. A 2.1
CC kb cDNA clone was obtd. Analysis of additional clones in the MM6 cDNA
CC library revealed a second sequence that was identical to the 2.1 kb cDNA
CC sequence first obtd. from the 5' UTR through the putative seventh
CC transmembrane domain but contained a different cytoplasmic tail. The
CC second sequence appears to represent alternative splicing of the carboxyl
CC -terminal tail of the MCP-1R protein. The two sequences are denoted MCP-
CC 1RA and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature MCP-

```
CC   1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB has a mol.
CC   wt. of about 41,000 daltons. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 374 AA;

  Query Match             100.0%;  Score 1970;  DB 2;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-215;
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374


RESULT 2
AAG80107
ID   AAG80107 standard; protein; 374 AA.
XX
AC   AAG80107;
XX
DT   17-JAN-2002  (first entry)
XX
DE   Human CCR2a protein.
XX
KW   Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW   inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW   chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW   antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW   antirheumatic; antiarthritic.
XX
OS   Homo sapiens.
XX
```

PN WO200172830-A2.
XX
PD 04-OCT-2001.
XX
PF 02-APR-2001; 2001WO-EP003708.
XX
PR 31-MAR-2000; 2000DE-01016013.
XX
PA (IPFP-) IPF PHARM GMBH.
PA (FORS/) FORSSMANN U.
XX
PI Forssmann W, Adermann K, Heitland A, Spodsberg N;
XX
DR WPI; 2001-626256/72.
XX
PT Diagnostic agent containing two or more receptor-specific ligands, useful
PT for detecting tumors, inflammation etc., also therapeutic use of ligand
PT inhibitors.
XX
PS Disclosure; Page 9; 26pp; German.
XX
CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antiasthmatic,
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC constellation of chemokine receptors (CR), which control migration and
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention
XX
SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.1e-215;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
```

```
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
                    ||||||||||||||
Db        361 GRAPEASLQDKEGA 374
```

RESULT 3
ABU09083
ID ABU09083 standard; protein; 374 AA.
XX
AC ABU09083;
XX
DT 23-JUL-2003 (first entry)
XX
DE Human chemokine receptor-2 (CKR-2) polypeptide.
XX
KW Human; thymus expressed chemokine; TECK; chemokine; MIP-3alpha; receptor;
KW MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma;
KW monocyte/dendritic cell receptor for chemokine; inflammatory condition;
KW abnormal physiology; abnormal proliferation; degeneration; atrophy;
KW antiinflammatory; antiasthmatic; cytostatic; chemokine receptor-2; CKR-2.
XX
OS Homo sapiens.
XX
PN US2003018167-A1.
XX
PD 23-JAN-2003.
XX
PF 03-JAN-2002; 2002US-00039659.
XX
PR 05-JUL-1996; 96US-0021664P.
PR 11-OCT-1996; 96US-0028329P.
PR 04-JUN-1997; 97US-0048593P.
PR 03-JUL-1997; 97US-00887977.
XX
PA (SCHE) SCHERING CORP.
XX
PI Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;
XX
DR WPI; 2003-416900/39.
XX
PT New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCCR, useful
PT for treating conditions associated with abnormal physiology or
PT development, including inflammatory conditions (e.g. asthma), and
PT abnormal proliferation.
XX
PS Disclosure; Page 9-10; 54pp; English.

```
XX
CC   The invention relates to nucleic acids encoding the chemokines TECK, MIP-
CC   3alpha, MIP-3beta, DC CR and M/DC CR. The polypeptide sequences are
CC   useful in isolating DNA clones encoding the chemokines, for generating
CC   antibodies, and for predicting oligonucleotides for screening a library
CC   to isolate species variants. A nucleic acid encoding a chemokine
CC   polypeptide can be used to identify genes, mRNA and cDNA species which
CC   encode related or homologous ligands, as well as DNA encoding homologous
CC   proteins from different species. The chemokines and antibodies which bind
CC   to the polypeptides are useful in the treatment of conditions associated
CC   with abnormal physiology or development, including inflammatory
CC   conditions such as asthma, abnormal proliferation, regeneration,
CC   degeneration and atrophy. This sequence represents the human chemokine
CC   receptor-2 (CKR-2) polypeptide, used in the scope of the invention
XX
SQ   Sequence 374 AA;

  Query Match             100.0%;  Score 1970;  DB 6;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-215;
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374


RESULT 4
ADD44861
ID   ADD44861 standard; protein; 374 AA.
XX
AC   ADD44861;
XX
DT   29-JAN-2004  (first entry)
```

XX
DE Human Protein P41597, SEQ ID NO 10292.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P41597.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed

```
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 374 AA;

  Query Match             100.0%;  Score 1970;  DB 7;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-215;
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374


RESULT 5
ADD44865
ID   ADD44865 standard; protein; 374 AA.
XX
AC   ADD44865;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein P41597, SEQ ID NO 10296.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
```

XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P41597.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 7; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.1e-215;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

```
Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374
```

RESULT 6
ADP65146
ID   ADP65146 standard; protein; 374 AA.
XX
AC   ADP65146;
XX
DT   12-AUG-2004 (first entry)
XX
DE   Human chemokine (C-C motif) receptor 2, isoform A, chemokine (C-C).
XX
KW   autoimmune disease; arthritide; gene expression analysis;
KW   rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW   antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
KW   immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
KW   fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW   immune; human.
XX
OS   Homo sapiens.
XX
PN   WO2003072827-A1.
XX
PD   04-SEP-2003.
XX
PF   31-OCT-2002; 2002WO-US035433.
XX
PR   31-OCT-2001; 2001US-0336220P.
XX
PA   (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX
PI   Hirsch R, Thorton SL;
XX

DR WPI; 2003-712740/67.
DR GENBANK; NP_000638.
XX
PT Diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
XX
PS Disclosure; Page; 56pp; English.
XX
CC The invention relates to a novel method for diagnosing and analysing
CC autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritides. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.
XX
SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 7; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.1e-215;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374
```

RESULT 7
ADO29221
ID ADO29221 standard; protein; 374 AA.
XX
AC ADO29221;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human GPCR CCR2, SEQ ID NO:322.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO2004040000-A2.
XX
PD 13-MAY-2004.
XX
PF 09-SEP-2003; 2003WO-US028226.
XX
PR 09-SEP-2002; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX
PA (PRIM-) PRIMAL INC.
XX
PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX

DR WPI; 2004-390329/36.
DR N-PSDB; ADO29829.
XX
PT Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
PS Claim 151; SEQ ID NO 322; 542pp; English.
XX
CC The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the trasngenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 8; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.1e-215;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
                ||||||||||||||
Db        361 GRAPEASLQDKEGA 374
```

RESULT 8
ADQ67847
ID ADQ67847 standard; protein; 374 AA.
XX
AC ADQ67847;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human chemokine receptor CCR-2.
XX
KW Human; receptor; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW chemokine receptor; DCCR; dendritic cell receptor for chemokine; M/DCCR;
KW Monocyte/dendritic cell receptor for chemokine; abnormal physiology;
KW development; inflammatory condition; asthma.
XX
OS Homo sapiens.
XX
PN US2004137578-A1.
XX
PD 15-JUL-2004.
XX
PF 09-JAN-2004; 2004US-00754071.
XX
PR 05-JUL-1996; 96US-0021664P.
PR 11-OCT-1996; 96US-0028329P.
PR 04-JUN-1997; 97US-0048593P.
PR 03-JUL-1997; 97US-00887977.
PR 03-JAN-2002; 2002US-00039659.
XX
PA (WANG/) WANG W.
PA (GISH/) GISH K C.
PA (SCHA/) SCHALL T J.
PA (VICA/) VICARI A.
PA (ZLOT/) ZLOTNIK A.
XX
PI Wang W, Gish KC, Schall TJ, Vicari A, Zlotnik A;
XX

DR WPI; 2004-533376/51.
XX
PT New substantially pure or isolated Thymus Expressed Chemokine (TECK), useful for treating conditions associated with abnormal physiology or development, including inflammatory conditions, e.g. asthma.
XX
PS Disclosure; SEQ ID NO 14; 54pp; English.
XX
CC The invention relates to a substantially pure or isolated polypeptide comprises the mature protein of human TECK (thymus expressed chemokine) whose full length sequence appears as ADQ67837. Also included are an isolated or recombinant nucleic acid encoding mature TECK, an expression vector comprising the nucleic acid, a host cell comprising the expression vector and a method for producing the polypeptide. Also disclosed are the mouse TECK cDNA and protein, human chemokines MIP-3alpha and MIP-3beta (and their encoding cDNAs), and the cDNAs and encoded proteins corresponding to human chemokine receptors DCCR (dendritic cell receptor for chemokine) and M/DCCR (Monocyte/dendritic cell receptor for chemokine). The polypeptide is useful for treating conditions associated with abnormal physiology or development, including inflammatory conditions, e.g. asthma. The present sequence represents a human chemokine receptor showing sequence similarity to M/DCCR.
XX
SQ Sequence 374 AA;

Query Match 100.0%; Score 1970; DB 8; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.1e-215;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374
```

RESULT 9
ABG92881
ID ABG92881 standard; peptide; 344 AA.
XX
AC ABG92881;
XX
DT 19-NOV-2002 (first entry)
XX
DE Class I receptors WSXWS motif.
XX
KW Immunoglobulin; variable heavy chain; variable light chain; human;
KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
KW immunologic deficiency syndrome; blood protein disorder; nephritis;
KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
KW Pneumocystis carnii infection; cardiovascular disorder; atherosclerosis;
KW lymphocytopenia.
XX
OS Synthetic.
XX
PN WO200264612-A2.
XX
PD 22-AUG-2002.
XX
PF 08-FEB-2002; 2002WO-US003634.
XX
PR 09-FEB-2001; 2001US-00779880.
PR 09-FEB-2001; 2001WO-US004153.
PR 12-JUN-2001; 2001US-0297257P.
PR 08-AUG-2001; 2001US-0310458P.
PR 12-OCT-2001; 2001US-0328447P.
PR 21-DEC-2001; 2001US-0341725P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Roschke V, Rosen CA, Ruben SM;
XX
DR WPI; 2002-643455/69.
XX
PT New human G-protein Chemokine Receptor gene (HDGNR10) useful for
PT treating, preventing, ameliorating or monitoring diseases or disorders
PT associated with aberrant expression of HDGNR10 e.g. cancer.
XX
PS Example 17; Page 386; 562pp; English.
XX
CC The invention describes an isolated polynucleotide encoding a first
CC antibody at least 95-100% identical to a second antibody consisting of an
CC amino acid sequence comprising at least one, two or three CDR regions of
CC a variable heavy (VH) or variable light (VL) domain of the antibody
CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,
CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
CC is useful treating, preventing, ameliorating, prognosing or monitoring

CC cancers or other diseases or disorders e.g. immunologic deficiency
CC syndromes such as blood protein disorders and ataxia telangiectasia,
CC inflammation associated disorders such as endotoxin lethality, nephritis
CC and inflammatory bowel disease, conditions associated with an increase in
CC certain haematopoietic cells such as histiocytosis, defective or aberrant
CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
CC an infectious disease, an autoimmune disease such as Addison's disease,
CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
CC poxvirus infection, a Pneumocystis carnii infection, Kaposi's sarcoma,
CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
CC disease or disorder associated with aberrant expression of novel human G-
CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
CC sequence of the WSXWS motif found in class I receptors
XX
SQ Sequence 344 AA;

Query Match 92.5%; Score 1823; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.5e-198;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||
Db        301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
```

RESULT 10
ABU61655
ID ABU61655 standard; protein; 344 AA.
XX
AC ABU61655;
XX
DT 08-AUG-2003 (first entry)
XX
DE Human monocyte chemoattractant protein 1 (MCP-1) receptor.
XX
KW Human; G-protein chemokine receptor; receptor; HDGNR10; MCP-1;

KW 7-transmembrane receptor; monocyte chemoattractant protein 1.
XX
OS Homo sapiens.
XX
PN US2003023044-A1.
XX
PD 30-JAN-2003.
XX
PF 03-SEP-2002; 2002US-00232686.
XX
PR 06-JUN-1995; 95US-00466343.
PR 18-NOV-1998; 98US-00195662.
PR 25-JUN-1999; 99US-00339912.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Li Y, Ruben SM;
XX
DR WPI; 2003-456307/43.
XX
PT Producing an antibody, involves immunizing an animal with a polypeptide
PT or with a polypeptide encoded by the human G-protein chemokine receptor
PT clone in ATCC 97183, and recovering the antibody.
XX
PS Disclosure; Fig 2; 23pp; English.
XX
CC The invention relates to a method of producing an antibody, involving
CC immunising an animal with a human G-protein chemokine receptor (HDGNR10)
CC polypeptide (also referred to as a human 7-transmembrane receptor) and
CC recovering an antibody which binds the polypeptide. The method is useful
CC for producing an antibody which binds specifically to the human G-protein
CC chemokine receptor polypeptide. This sequence represents the monocyte
CC chemoattractant protein 1 (MCP-1) receptor which shares homology with the
CC HDGNR10 polypeptide of the invention
XX
SQ Sequence 344 AA;

Query Match 92.5%; Score 1823; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.5e-198;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240
```

```
Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
```

RESULT 11
ADF72129
ID ADF72129 standard; protein; 344 AA.
XX
AC ADF72129;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human G-protein chemokine receptor (CCR5) ligand MCP-1.
XX
KW cytostatic; CCR5 modulator; antibody; G-protein chemokine receptor; CCR5;
KW cancer detection; cancer diagnosis; cancer prognosis; cancer monitoring;
KW cancer; hyperproliferative disorder; human; HDGNR10; ligand; MCP-1.
XX
OS Homo sapiens.
XX
PN US2003166024-A1.
XX
PD 04-SEP-2003.
XX
PF 01-MAY-2002; 2002US-00135839.
XX
PR 09-FEB-2000; 2000US-0181258P.
PR 09-MAR-2000; 2000US-0187999P.
PR 22-SEP-2000; 2000US-0234336P.
PR 09-FEB-2001; 2001US-00779879.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX
DR WPI; 2003-898066/82.
XX
PT New polypeptide comprising domains of an antibody that binds G-protein
PT chemokine receptor CCR5 is useful to detect, diagnose, prognose or
PT monitor cancers and other hyperproliferative disorders and to treat or
PT prevent a disease or disorder.
XX
PS Disclosure; SEQ ID NO 9; 179pp; English.
XX
CC The invention describes a new isolated polynucleotide that encodes an
CC antibody (AB1) comprising an amino acid sequence of at least one, two or
CC three complementarity determining regions (CDR) of a heavy chain variable
CC (VH) domain of an antibody (AB2) that immunospecifically binds to a G-
CC protein chemokine receptor (CCR5), at least one, two or three CDR regions
CC of a light chain varaible (VL) domain of AB2 or at least one, two or
CC three CDR regions of both a VH and a VL domain of AB2. The antibody is
CC useful for detecting, diagnosing, prognosing or monitoring cancers and

```
CC   other hyperproliferative disorders and for treating, preventing or
CC   ameliorating a disease or disorder. This is the amino acid sequence of
CC   MCP-1, a ligand of human G protein chemokine receptor (CCR5) HDGNR10.
XX
SQ   Sequence 344 AA;

  Query Match             92.5%;  Score 1823;  DB 7;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-198;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||
Db        301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344


RESULT 12
ADP86217
ID   ADP86217 standard; protein; 344 AA.
XX
AC   ADP86217;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human MCP-1 receptor protein.
XX
KW   G-protein chemokine receptor; HDGNR10; CCR5; haematopoiesis;
KW   wound healing; coagulation; angiogenesis; tumour; chronic infection;
KW   leukaemia; T-cell mediated autoimmune diseases; parasitic infection;
KW   psoriasis; allergy; anaphylaxis; atherogenesis; malignancy; inflammation;
KW   prostaglandin-independent fever; bone marrow failure; silicosis;
KW   sarcoidosis; rheumatoid arthritis; shock; hyper-eosinophilic syndrome;
KW   human; MCP-1 receptor ; receptor.
XX
OS   Homo sapiens.
XX
PN   US6743594-B1.
XX
```

PD 01-JUN-2004.
XX
PF 11-FEB-2000; 2000US-00502784.
XX
PR 06-JUN-1995; 95US-00466343.
PR 18-NOV-1998; 98US-00195662.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Li Y, Ruben SM;
XX
DR WPI; 2004-459648/43.
XX
PT Screening compounds binding to G-protein chemokine receptor HDGNR10,
PT involves contacting test compound with polypeptide of HDGRN10, and
PT observing binding of test compound to polypeptide.
XX
PS Disclosure; SEQ ID NO 9; 26pp; English.
XX
CC The invention relates to a method for screening compounds which bind the
CC G-protein chemokine receptor HDGNR10 (CCR5). Compounds identified by the
CC method of the invention are useful for stimulating haematopoiesis, wound
CC healing, coagulation, angiogenesis, for treating solid tumours, chronic
CC infections, leukaemia, T-cell mediated autoimmune diseases, parasitic
CC infections, psoriasis and for stimulating growth factor activity. The
CC compounds are also useful for treating allergy, anaphylaxis,
CC atherogenesis, malignancy, chronic and acute inflammation, histamine and
CC IgE-mediated allergic reactions, prostaglandin-independent fever, bone
CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis, shock and
CC hyper-eosinophilic syndrome. The present sequence is a human MCP-1
CC receptor protein. This sequence is used in the invention.
XX
SQ Sequence 344 AA;

Query Match 92.5%; Score 1823; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.5e-198;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy          78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy         138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy         198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy         258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300
```

```
Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||||
Db        301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
```

RESULT 13
AAB46859
ID AAB46859 standard; protein; 329 AA.
XX
AC AAB46859;
XX
DT 16-AUG-2001 (revised)
DT 02-AUG-2001 (revised)
DT 04-MAY-2001 (first entry)
XX
DE Human MCP-1 receptor protein fragment.
XX
KW HDGNR10; human; G-protein chemokine receptor; antiinflammatory;
KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
KW cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;
KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;
KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
KW hyper-eosinophilic syndrome; vulnerary.
XX
OS Homo sapiens.
XX
PN US2001000241-A1.
XX
PD 12-APR-2001.
XX
PF 29-NOV-2000; 2000US-00725285.
XX
PR 06-JUN-1995; 95US-00466343.
PR 18-NOV-1998; 98US-00195662.
PR 25-JUN-1999; 99US-00339912.
XX
PA (LIYY/) LI Y.
PA (RUBE/) RUBEN S M.
XX
PI Li Y, Ruben SM;
XX
DR WPI; 2001-226317/23.
XX
PT New human G-protein chemokine receptor polypeptides and polynucleotides,
PT useful for identifying (ant)agonists to the G-protein chemokine receptor.
XX
PS Disclosure; Page 16-17; 22pp; English.
XX
CC This invention describes a novel receptor polypeptide (I) selected from
CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the
CC specification; and (ii) a polypeptide encoded by the cDNA contained in a
CC plasmid, and fragments, analogs and derivatives of the polypeptide. The

CC products of the invention have antiinflammatory, immunomodulatory, anticoagulant, antiallergic, immunosuppressive, vulnerary, cytostatic, antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic activity and can be used for gene therapy. The G-protein chemokine receptors, HDGNR10, (I) are useful for screening for compounds which activate or inhibit activation of (I). The products of the invention can also be used for stimulating haematopoiesis, wound healing, coagulation, angiogenesis, treating solid tumours, chronic infections, leukemia, T-cell mediated autoimmune diseases, parasitic infections, psoriasis, and stimulating growth factor activity. HDGNR10 is useful for treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute inflammation, histamine and immunoglobulin E (IgE)-mediated allergic reactions, prostaglandin-independent fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-eosinophilic syndrome. (N.B. This record was resubmitted to correct errors in the keyword formatting)
XX
SQ Sequence 329 AA;

Query Match 87.7%; Score 1727.5; DB 4; Length 329;
Best Local Similarity 95.6%; Pred. No. 1.8e-187;
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

```
Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI--------------- 105

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||
Db        286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329
```

RESULT 14
ABB81055
ID ABB81055 standard; protein; 329 AA.
XX
AC ABB81055;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human MCP-1 receptor.

XX
KW 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10;
KW G-protein chemokine receptor; haematopoietic; immunosuppressant;
KW antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic;
KW antirheumatic; antiarthritic; gene therapy; human; MCP-1; receptor.
XX
OS Homo sapiens.
XX
PN US2002076745-A1.
XX
PD 20-JUN-2002.
XX
PF 18-NOV-1998; 98US-00195662.
XX
PR 06-JUN-1995; 95US-00466343.
XX
PA (LIYY/) LI Y.
PA (RUBE/) RUBEN S M.
XX
PI Li Y, Ruben SM;
XX
DR WPI; 2002-598724/64.
XX
PT New polynucleotide encoding a human G protein chemokine receptor HDGNR10,
PT useful e.g. for treating tumors.
XX
PS Example; Fig 2; 22pp; English.
XX
CC The invention relates to a novel human 7-transmembrane receptor, HDGNR10,
CC which has been identified as a G-protein chemokine receptor. The GPCR
CC HDGNR10 polypeptide can be expressed by standard recombinant methodology.
CC Compounds that activate or inhibit the receptor polypeptide, optionally
CC expressed from DNA in gene therapy vectors, are used to treat diseases
CC that require: (a) activation of the receptor (e.g. stimulation of
CC haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune
CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the
CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis
CC etc). The present sequence represents a human MCP-1 receptor used in
CC comparison studies with the HDGNR10 receptor
XX
SQ Sequence 329 AA;

Query Match 87.7%; Score 1727.5; DB 5; Length 329;
Best Local Similarity 95.6%; Pred. No. 1.8e-187;
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

```
Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI--------------- 105

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165
```

```
Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||
Db        286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329
```

RESULT 15
ADR16266
ID ADR16266 standard; protein; 329 AA.
XX
AC ADR16266;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human MCP-1 receptor protein fragment.
XX
KW G-protein chemokine receptor; CCR5; HDGNR10; allergy; atherogenesis;
KW anaphylaxis; malignancy; inflammation; prostaglandin-independent fever;
KW bone marrow failure; silicosis; sarcoidosis; rheumatoid arthritis; shock;
KW hypereosinophilic syndrome; haematopoiesis; wound healing; coagulation;
KW angiogenesis; solid tumour; chronic infection; leukaemia;
KW autoimmune disease; parasitic infection; psoriasis; human;
KW MCP-1 receptor; receptor.
XX
OS Homo sapiens.
XX
PN US2004151719-A1.
XX
PD 05-AUG-2004.
XX
PF 04-MAR-2004; 2004US-00791905.
XX
PR 06-JUN-1995; 95US-00466343.
PR 18-NOV-1998; 98US-00195662.
PR 25-JUN-1999; 99US-00339912.
PR 11-FEB-2000; 2000US-00502783.
PR 23-APR-2002; 2002US-00127764.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Li Y, Ruben SM;
XX
DR WPI; 2004-580174/56.
XX
PT New isolated antibody that binds to an extracellular portion of human G-
PT protein chemokine receptor 5 (CCR5) (also known as HDGNR10), useful for
PT treating conditions such as allergies, cancers, and inflammation.
XX
PS Disclosure; SEQ ID NO 9; 23pp; English.

XX
CC The invention provides a human G-protein chemokine receptor (CCR5)
CC HDGNR10 polynucleotide, polypeptides, and antibodies. The antibody that
CC is an antagonist of HDGNR10 is potentially useful for preventing or
CC treating allergy, atherogenesis, anaphylaxis, malignancy, chronic and
CC acute inflammation, histamine and IgE-mediated allergic reactions,
CC prostaglandin-independent fever, bone marrow failure, silicosis,
CC sarcoidosis, rheumatoid arthritis, shock and hypereosinophilic syndrome.
CC The compounds that bind to and activate the receptor are potentially
CC useful for stimulating haematopoiesis, wound healing, coagulation and
CC angiogenesis, and in treating solid tumours, chronic infections,
CC leukaemia, T-cell mediated auto-immune diseases, parasitic infections and
CC psoriasis. The antibody may also be used as a diagnostic reagent. The
CC present sequence is a human MCP-1 receptor fragment (residues 18-361)
CC which shares homology with the G-protein chemokine receptor (CCR5)
CC HDGNR10 of the invention.
XX
SQ Sequence 329 AA;

Query Match 87.7%; Score 1727.5; DB 8; Length 329;
Best Local Similarity 95.6%; Pred. No. 1.8e-187;
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

```
Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              |||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI--------------- 105

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||
Db        286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329
```

Search completed: March 31, 2005, 14:03:52
Job time : 178 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 31, 2005, 13:58:29 ; Search time 43 Seconds
(without alignments)
649.273 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 1970
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1970	100.0	374	1	US-08-450-393A-2	Sequence 2, Appli
2	1970	100.0	374	3	US-08-446-669-2	Sequence 2, Appli
3	1970	100.0	374	4	US-10-039-659A-14	Sequence 14, Appl
4	1970	100.0	374	4	US-09-625-573-2	Sequence 2, Appli
5	1970	100.0	374	5	PCT-US95-00476-2	Sequence 2, Appli
6	1970	100.0	387	4	US-09-949-016-11222	Sequence 11222, A
7	1823	92.5	344	3	US-08-466-343D-9	Sequence 9, Appli
8	1823	92.5	344	4	US-09-502-784A-9	Sequence 9, Appli
9	1727.5	87.7	329	4	US-09-502-783A-9	Sequence 9, Appli
10	1727.5	87.7	329	4	US-09-339-912A-9	Sequence 9, Appli
11	1727.5	87.7	329	4	US-09-195-662A-9	Sequence 9, Appli

12	1651.5	83.8	360	1	US-08-450-393A-4	Sequence 4, Appli
13	1651.5	83.8	360	3	US-08-446-669-4	Sequence 4, Appli
14	1651.5	83.8	360	3	US-09-045-583-50	Sequence 50, Appl
15	1651.5	83.8	360	4	US-09-534-185-50	Sequence 50, Appl
16	1651.5	83.8	360	4	US-09-131-827A-2	Sequence 2, Appli
17	1651.5	83.8	360	4	US-09-625-573-4	Sequence 4, Appli
18	1651.5	83.8	360	5	PCT-US95-00476-4	Sequence 4, Appli
19	1651.5	83.8	377	4	US-09-949-016-11221	Sequence 11221, A
20	1650.5	83.8	360	4	US-09-131-827A-20	Sequence 20, Appl
21	1645.5	83.5	360	4	US-08-833-752-7	Sequence 7, Appli
22	1645.5	83.5	360	4	US-09-938-719-7	Sequence 7, Appli
23	1645.5	83.5	360	4	US-09-939-226B-7	Sequence 7, Appli
24	1645.5	83.5	360	4	US-09-826-509-473	Sequence 473, App
25	1614.5	82.0	360	3	US-09-045-583-51	Sequence 51, Appl
26	1614.5	82.0	360	4	US-09-534-185-51	Sequence 51, Appl
27	1589.5	80.7	347	1	US-08-461-244-3	Sequence 3, Appli
28	1236	62.7	352	3	US-09-517-605-5	Sequence 5, Appli
29	1234	62.6	354	3	US-08-724-984A-2	Sequence 2, Appli
30	1230	62.4	352	3	US-09-045-583-52	Sequence 52, Appl
31	1230	62.4	352	4	US-09-534-185-52	Sequence 52, Appl
32	1224	62.1	352	3	US-09-087-232A-13	Sequence 13, Appl
33	1224	62.1	352	3	US-08-861-105-14	Sequence 14, Appl
34	1224	62.1	352	3	US-08-575-967A-2	Sequence 2, Appli
35	1224	62.1	352	4	US-08-833-752-5	Sequence 5, Appli
36	1224	62.1	352	4	US-09-502-783A-2	Sequence 2, Appli
37	1224	62.1	352	4	US-09-796-202-1	Sequence 1, Appli
38	1224	62.1	352	4	US-09-938-719-5	Sequence 5, Appli
39	1224	62.1	352	4	US-09-502-784A-2	Sequence 2, Appli
40	1224	62.1	352	4	US-09-339-912A-2	Sequence 2, Appli
41	1224	62.1	352	4	US-08-771-276-2	Sequence 2, Appli
42	1224	62.1	352	4	US-08-771-276-20	Sequence 20, Appl
43	1224	62.1	352	4	US-09-939-226B-5	Sequence 5, Appli
44	1224	62.1	352	4	US-09-195-662A-2	Sequence 2, Appli
45	1218	61.8	352	4	US-09-826-509-477	Sequence 477, App

ALIGNMENTS

```
RESULT 1
US-08-450-393A-2
; Sequence 2, Application US/08450393A
; Patent No. 5707815
;  GENERAL INFORMATION:
;    APPLICANT:  Charo, Israel
;    APPLICANT:  Coughlin, Shaun
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/450,393A
;       FILING DATE:  May 25, 1995
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Cserr, Luann
;       REGISTRATION NUMBER:  31,822
;       REFERENCE/DOCKET NUMBER:  UCAL-237/02US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-843-5165
;       TELEFAX:  415-8857-0663
;       TELEX:  380816CooleyPA
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  374 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-450-393A-2

  Query Match             100.0%;  Score 1970;  DB 1;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-150;
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374
```

```
RESULT 2
US-08-446-669-2
; Sequence 2, Application US/08446669
; Patent No. 6132987
;  GENERAL INFORMATION:
;    APPLICANT:  Charo, Israel
;    APPLICANT:  Coughlin, Shaun
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,669
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Neeley, Richard
;      REGISTRATION NUMBER:  30,092
;      REFERENCE/DOCKET NUMBER:  UCAL-237/01US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5000
;      TELEFAX:  415-857-0663
;      TELEX:  380816CooleyPA
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  374 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-446-669-2

  Query Match             100.0%;  Score 1970;  DB 3;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-150;
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
```

```
Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374
```

RESULT 3
US-10-039-659A-14
; Sequence 14, Application US/10039659A
; Patent No. 6723520
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei
; APPLICANT: Gish, Kurt C.
; APPLICANT: Schall, Thomas J.
; APPLICANT: Vicari, Alain P.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Antibodies that bind chemokine TECK
; FILE REFERENCE: DX0589K1B US
; CURRENT APPLICATION NUMBER: US/10/039,659A
; CURRENT FILING DATE: 2002-01-03
; PRIOR APPLICATION NUMBER: US 08/887,977
; PRIOR FILING DATE: 1997-07-03
; PRIOR APPLICATION NUMBER: US 60/021,664
; PRIOR FILING DATE: 1996-07-05
; PRIOR APPLICATION NUMBER: US 60/028,329
; PRIOR FILING DATE: 1996-10-11
; PRIOR APPLICATION NUMBER: US 60/048,593
; PRIOR FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-659A-14

Query Match 100.0%; Score 1970; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.3e-150;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy         121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy         181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy         241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy         301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy         361 GRAPEASLQDKEGA 374
                ||||||||||||||
Db         361 GRAPEASLQDKEGA 374
```

RESULT 4
US-09-625-573-2
; Sequence 2, Application US/09625573
; Patent No. 6730301
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/625,573
; FILING DATE: 25-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US

```
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-843-5000
;             TELEFAX: 415-857-0663
;             TELEX: 380816CooleyPA
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 374 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-625-573-2

  Query Match             100.0%;  Score 1970;  DB 4;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-150;
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374


RESULT 5
PCT-US95-00476-2
; Sequence 2, Application PC/TUS9500476
;  GENERAL INFORMATION:
;    APPLICANT:  The Regents of the University of California
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Robbins, Berliner & Carson
;      STREET:  201 N. Figueroa Street, 5th Floor
```

```
;       CITY:  Los Angeles
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  90012-2628
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/00476
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Berliner, Robert
;       REGISTRATION NUMBER:  20,121
;       REFERENCE/DOCKET NUMBER:  5555-291
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  310-977-1001
;       TELEFAX:  310-977-1003
;       TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  374 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US95-00476-2

  Query Match             100.0%;  Score 1970;  DB 5;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-150;
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
```

```
Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374


RESULT 6
US-09-949-016-11222
; Sequence 11222, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11222
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-11222

  Query Match             100.0%;  Score 1970;  DB 4;  Length 387;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-150;
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 73

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 133

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 193

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 253

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 313

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        314 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 373

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        374 GRAPEASLQDKEGA 387


RESULT 7
US-08-466-343D-9
; Sequence 9, Application US/08466343D
; Patent No. 6025154
;  GENERAL INFORMATION:
;    APPLICANT:  LI, Yi
;    TITLE OF INVENTION:  POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
;    TITLE OF INVENTION:  CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,343D
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEFFE, ERIC K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.1150000/EKS/KLM
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  344 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-466-343D-9

  Query Match             92.5%;  Score 1823;  DB 3;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-138;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy         138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy         198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy         258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy         318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
                |||||||||||||||||||||||||||||||||||||||||||
Db         301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
```

RESULT 8
US-09-502-784A-9
; Sequence 9, Application US/09502784A
; Patent No. 6743594
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Methods of Screening Using Human G-Protein
; TITLE OF INVENTION: Chemokine Receptor HDGNR10 (CCR5)
; FILE REFERENCE: 1488.1150005
; CURRENT APPLICATION NUMBER: US/09/502,784A
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 9
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-502-784A-9

```
  Query Match             92.5%;  Score 1823;  DB 4;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-138;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy          78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy         138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy         198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy         258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy         318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
                |||||||||||||||||||||||||||||||||||||||||||
Db         301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
```

RESULT 9
US-09-502-783A-9
; Sequence 9, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)
; TITLE OF INVENTION: HDGNR10
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-502-783A-9

Query Match 87.7%; Score 1727.5; DB 4; Length 329;
Best Local Similarity 95.6%; Pred. No. 9.8e-131;
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

```
Qy          18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy          78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
               |||||||||||||||||||||||||||||||||||||||||
Db          61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI---------------- 105

Qy         138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy         198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||
Db        286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329


RESULT 10
US-09-339-912A-9
; Sequence 9, Application US/09339912A
; Patent No. 6759519
; GENERAL INFORMATION:
;  APPLICANT:   Li, Yi
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION:   Antibodies to Human G-Protein Chemokine Receptor
HDGNR10
;  TITLE OF INVENTION:  (CCR5 Receptor)
;  FILE REFERENCE:   1488.1150003
;  CURRENT APPLICATION NUMBER: US/09/339,912A
;  CURRENT FILING DATE:  1999-06-25
;  PRIOR APPLICATION NUMBER:   09/195,662
;  PRIOR FILING DATE:   1998-11-18
;  PRIOR APPLICATION NUMBER:   08/466,343
;  PRIOR FILING DATE:   1995-06-06
;  NUMBER OF SEQ ID NOS:   9
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Protein
US-09-339-912A-9

  Query Match             87.7%;  Score 1727.5;  DB 4;  Length 329;
  Best Local Similarity   95.6%;  Pred. No. 9.8e-131;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels   15;  Gaps    1;

Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI--------------- 105

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
                |||||||||||||||||||||||||||||||||||||||||||||
Db        286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329


RESULT 11
US-09-195-662A-9
; Sequence 9, Application US/09195662A
; Patent No. 6800729
; GENERAL INFORMATION:
;  APPLICANT:   Li, Yi
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION:   Human G-Protein Chemokine Receptor HDGNR10 (CCR5
Receptor)
;  FILE REFERENCE:   1488.1150002
;  CURRENT APPLICATION NUMBER: US/09/195,662A
;  CURRENT FILING DATE:  1998-11-18
;  PRIOR APPLICATION NUMBER:   08/466,343
;  PRIOR FILING DATE:   1995-06-06
;  NUMBER OF SEQ ID NOS:   9
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Protein
US-09-195-662A-9

  Query Match             87.7%;  Score 1727.5;  DB 4;  Length 329;
  Best Local Similarity   95.6%;  Pred. No. 9.8e-131;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels   15;  Gaps    1;

Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI--------------- 105

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||||
Db        286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329
```

```
RESULT 12
US-08-450-393A-4
; Sequence 4, Application US/08450393A
; Patent No. 5707815
;  GENERAL INFORMATION:
;    APPLICANT:  Charo, Israel
;    APPLICANT:  Coughlin, Shaun
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,393A
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cserr, Luann
;      REGISTRATION NUMBER:  31,822
;      REFERENCE/DOCKET NUMBER:  UCAL-237/02US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5165
;      TELEFAX:  415-8857-0663
;      TELEX:  380816CooleyPA
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  360 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-450-393A-4

  Query Match             83.8%;  Score 1651.5;  DB 1;  Length 360;
  Best Local Similarity   95.5%;  Pred. No. 1.3e-124;
  Matches  319;  Conservative    3;  Mismatches    5;  Indels    7;  Gaps    3;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
                |||||||||||||   |:|   ||    |:  |:
Db        301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV 334


RESULT 13
US-08-446-669-4
; Sequence 4, Application US/08446669
; Patent No. 6132987
;  GENERAL INFORMATION:
;    APPLICANT:  Charo, Israel
;    APPLICANT:  Coughlin, Shaun
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,669
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Neeley, Richard
;      REGISTRATION NUMBER:  30,092
;      REFERENCE/DOCKET NUMBER:  UCAL-237/01US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5000
;      TELEFAX:  415-857-0663
;      TELEX:  380816CooleyPA
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  360 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-446-669-4
```

```
  Query Match             83.8%;  Score 1651.5;  DB 3;  Length 360;
  Best Local Similarity   95.5%;  Pred. No. 1.3e-124;
  Matches  319;  Conservative    3;  Mismatches    5;  Indels    7;  Gaps    3;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
              |||||||||||||   |:|   ||    |:  |:
Db        301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV 334


RESULT 14
US-09-045-583-50
; Sequence 50, Application US/09045583
; Patent No. 6287805
;  GENERAL INFORMATION:
;    APPLICANT:  Graham, Gerard J. et al.
;    TITLE OF INVENTION:  No. 6287805el Molecules of the G Protein-Coupled
;    NUMBER OF SEQUENCES:  56
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/045,583
;      FILING DATE:  20-MAR-98
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  MNI-044
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  360 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-09-045-583-50

  Query Match             83.8%;  Score 1651.5;  DB 3;  Length 360;
  Best Local Similarity   95.5%;  Pred. No. 1.3e-124;
  Matches  319;  Conservative    3;  Mismatches    5;  Indels    7;  Gaps    3;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
              |||||||||||||   |:|   ||    |:  |:
Db        301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV 334


RESULT 15
US-09-534-185-50
; Sequence 50, Application US/09534185
; Patent No. 6403767
;   GENERAL INFORMATION:
;        APPLICANT: Graham, Gerard J. et al.
;        TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
;                            Heptahelical Receptor Superfamily and Uses
;                            Therefor
;        NUMBER OF SEQUENCES: 56
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: LAHIVE & COCKFIELD, LLP
```

```
;              STREET: 28 State Street
;              CITY: Boston
;              STATE: Massachusetts
;              COUNTRY: USA
;              ZIP: 02109
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.25
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/534,185
;              FILING DATE: 24-Mar-2000
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 09/045,583
;              FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Mandragouras, Amy E.
;              REGISTRATION NUMBER: 36,207
;              REFERENCE/DOCKET NUMBER: MNI-044
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (617)227-7400
;              TELEFAX: (617)742-4214
;    INFORMATION FOR SEQ ID NO: 50:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 360 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: peptide
;         FRAGMENT TYPE: internal
;         SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

  Query Match             83.8%;  Score 1651.5;  DB 4;  Length 360;
  Best Local Similarity   95.5%;  Pred. No. 1.3e-124;
  Matches  319;  Conservative    3;  Mismatches    5;  Indels    7;  Gaps    3;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
```

```
Qy         301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
               ||||||||||||   |:|   ||    |:  |:
Db         301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV 334
```

Search completed: March 31, 2005, 14:08:41
Job time : 47 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 31, 2005, 13:57:49 ; Search time 46 Seconds
(without alignments)
782.284 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 1970
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1970	100.0	374	2	I38450	chemokine (C-C) re
2	1651.5	83.8	360	2	JC2443	chemokine (C-C) re
3	1224	62.1	352	2	A43113	chemokine (C-C) re
4	967.5	49.1	355	2	A45177	chemokine (C-C) re
5	960	48.7	359	2	I49341	MIP-1 alpha recept
6	902.5	45.8	355	2	I49339	macrophage inflamm
7	890.5	45.2	355	2	G02436	chemokine (C-C) re
8	833	42.3	360	2	JC4587	chemokine (C-C) re
9	831.5	42.2	360	2	A57160	chemokine (C-C) re
10	794.5	40.3	383	2	S55594	G protein-coupled
11	731	37.1	356	2	I49340	MIP-1 alpha recept
12	723	36.7	355	2	JC5067	G protein-coupled
13	704.5	35.8	354	2	I58186	probable G protein

14	698	35.4	355	2	JC4304	orphan G protein-c
15	644.5	32.7	344	2	JC5942	chemokine receptor
16	584	29.6	378	2	B55735	lymphocyte-specifi
17	575.5	29.2	378	2	A55735	G protein-coupled
18	570	28.9	378	2	A45680	G protein-coupled
19	554.5	28.1	369	2	JC5068	G protein-coupled
20	541.5	27.5	360	2	A53611	interleukin-8 rece
21	537	27.3	359	2	A48921	interleukin-8 rece
22	531	27.0	352	2	G00048	fusin (LESTRA) - c
23	530.5	26.9	353	2	S28787	neuropeptide Y/pep
24	529.5	26.9	355	2	JQ1231	interleukin-8 rece
25	528	26.8	352	2	A45747	neuropeptide Y/pep
26	526	26.7	358	2	A53752	interleukin-8 rece
27	526	26.7	367	2	JE0349	interferon-inducib
28	524.5	26.6	350	2	A39445	interleukin-8 rece
29	523	26.5	356	2	S42096	interleukin-8 rece
30	519	26.3	333	2	I65989	G protein-coupled
31	484	24.6	350	2	JN0621	G protein-coupled
32	480	24.4	359	2	A42656	angiotensin II rec
33	479.5	24.3	374	2	S42628	G protein-coupled
34	475	24.1	359	2	I51372	angiotensin II rec
35	473	24.0	359	2	JC2134	angiotensin II rec
36	472	24.0	359	2	JH0621	angiotensin II rec
37	471	23.9	359	2	S15403	angiotensin II rec
38	471	23.9	359	2	JQ1516	angiotensin II rec
39	469	23.8	359	2	JC1104	angiotensin II rec
40	468	23.8	359	2	S44425	angiotensin II rec
41	465	23.6	359	2	JC1194	angiotensin II rec
42	465	23.6	374	2	S32785	G protein-coupled
43	464	23.6	359	2	A48857	angiotensin II rec
44	461.5	23.4	372	2	S26667	G protein-coupled
45	460.5	23.4	327	2	S56162	MDCR15 protein - h

ALIGNMENTS

RESULT 1
I38450
chemokine (C-C) receptor 2, splice form A - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C;Accession: I38450
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38450
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <RES>

A;Cross-references: UNIPROT:P41597; EMBL:U03882; NID:g472555; PIDN:AAA19119.1;
PID:g472556
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein;
transmembrane protein
F;44-68/Domain: transmembrane #status predicted <TM1>
F;79-99/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;244-265/Domain: transmembrane #status predicted <TM6>
F;292-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;32-277,113-190/Disulfide bonds: #status predicted

Query Match 100.0%; Score 1970; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 1e-164;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374
```

RESULT 2
JC2443
chemokine (C-C) receptor 2, splice form B - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor;
monocyte chemotactin 1 receptor

C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: JC2443; I38463
R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor.
A;Reference number: JC2443; MUID:94324942; PMID:8048929
A;Accession: JC2443
A;Molecule type: mRNA
A;Residues: 1-360 <YAM>
A;Cross-references: UNIPROT:P41597; DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38463
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-360 <RES>
A;Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
F;43-70/Domain: transmembrane #status predicted <TM1>
F;81-100/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;207-226/Domain: transmembrane #status predicted <TM5>
F;244-268/Domain: transmembrane #status predicted <TM6>
F;287-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;113-190/Disulfide bonds: #status predicted

Query Match 83.8%; Score 1651.5; DB 2; Length 360;
Best Local Similarity 95.5%; Pred. No. 7.1e-137;
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

```
Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
```

```
Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
              |||||||||||||   |:|   ||    |:  |:
Db        301 NPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV 334
```

RESULT 3
A43113
chemokine (C-C) receptor 5 - human
N;Alternate names: C-C CKR-5; CCR5
C;Species: Homo sapiens (man)
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
C;Accession: A43113; S71808; A58834; A58832; G02653; A58833
R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor gene.
A;Reference number: A43113; MUID:96241590; PMID:8639485
A;Accession: A43113
A;Molecule type: mRNA
A;Residues: 1-352 <SAM1>
A;Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811
R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragosti, S.; Lapoumeroulie, C.; Cognaux, J.; Forceille, C.; Muyldermans, G.; Verhofstede, C.; Burtonboy, G.; Georges, M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Parmentier, M.
Nature 382, 722-725, 1996
A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the CCR-5 chemokine receptor gene.
A;Reference number: S71808; MUID:96345670; PMID:8751444
A;Accession: S71808
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 182-206;207-230 <SAM2>
A;Accession: A58834
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-184,'IKDSHLGAGPAAACHGHLLLGNPKNSASVSK' <SAM3>
A;Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A;Note: this frameshift mutation results in a non-functional receptor but confers a degree of resistance to HIV-1 infection; it has an allele frequency of 0.09 or more in some caucasian populations and may have had a selective advantage by conferring resistance to Yersinia plague infections
R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor selective for MIP-1alpha, MIP-1beta, and RANTES.

A;Reference number: A58832; MUID:96295970; PMID:8699119
A;Accession: A58832
A;Molecule type: mRNA
A;Residues: 1-352 <COM1>
A;Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R;Combadiere, C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01541
A;Accession: G02653
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-89,'L',91-352 <COM2>
A;Cross-references: EMBL:U57840
R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A;Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.
A;Reference number: A58833; MUID:96291862; PMID:8663314
A;Accession: A58833
A;Molecule type: mRNA
A;Residues: 1-352 <RAP>
A;Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A31767), and RANTES (see PIR:A28815).
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C-C) receptor 5 and T-cell surface glycoprotein CD4 (see PIR:RWHUT4).
C;Genetics:
A;Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
C;Function:
A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
A;Note: probably acts to control granulocyte proliferation and differentiation
C;Superfamily: vertebrate rhodopsin
C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;32-56/Domain: transmembrane #status predicted <TM1>
F;67-87/Domain: transmembrane #status predicted <TM2>
F;103-124/Domain: transmembrane #status predicted <TM3>
F;142-166/Domain: transmembrane #status predicted <TM4>
F;193-218/Domain: transmembrane #status predicted <TM5>
F;236-257/Domain: transmembrane #status predicted <TM6>
F;285-300/Domain: transmembrane #status predicted <TM7>
F;20-269,101-178/Disulfide bonds: #status predicted
F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 62.1%; Score 1224; DB 2; Length 352;
Best Local Similarity 76.3%; Pred. No. 1.8e-99;
Matches 235; Conservative 27; Mismatches 34; Indels 12; Gaps 3;

```
Qy          24 FDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
               :| :|    || | :|||| |:||||||||||||||||||:|||||||:|| :|||||
Db          10 YDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRLKSMTDIYL 69
```

```
Qy          82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
               |||||||| ||:|:| ||| || :| ||| ||:| |||| ||:| ||||||||||||||
Db          70 LNLAISDLFFLLTVPFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLA 129

Qy         142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
               :|||||||||||||||||||||||:||||||:||||||: |||   | |  :||    :
Db         130 VVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF 189

Qy         198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
               | || |:   |||||||||:|||||||||||||||||||||||||:||||||||||||
Db         190 WKNFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249

Qy         258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
               |||||:||||||||||:|| |:::|||| |||||||||||||||||||||||||:
Db         250 PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLL 309

Qy         317 -----HIA 319
                    |||
Db         310 VFFQKHIA 317
```

RESULT 4
A45177
chemokine (C-C) receptor 1 - human
N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A45177; I55671
R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor.
A;Reference number: A45177; MUID:93161416; PMID:7679328
A;Accession: A45177
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-355 <NEO>
A;Cross-references: UNIPROT:P32246; GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
R;Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha (MIP-1alpha)/RANTES receptor.
A;Reference number: I55671; MUID:93240122; PMID:7683036
A;Accession: I55671
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-355 <RES>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
C;Genetics:
A;Gene: GDB:CMKBR1; CMKR-1
A;Cross-references: GDB:138446; OMIM:601159
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin

C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein;
phosphoprotein; transmembrane protein
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-264/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status
predicted

Query Match 49.1%; Score 967.5; DB 2; Length 355;
Best Local Similarity 58.7%; Pred. No. 4.9e-77;
Matches 185; Conservative 47; Mismatches 72; Indels 11; Gaps 5;

```
Qy         12 NTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCK 71
              || |   : || |||    || | : :  |||||||||||||: | |||:||||:|:  |
Db          5 NTTED-YDTTTEFDYGDATPCQKVNERAFGAQLLPPLYSLVFVIGLVGNILVVLVLVQYK 63

Qy         72 KLKCLTDIYLLNLAISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIFF 130
              :|| :| ||||||||||||||| ||| |  :   ::||||:||||: :| |: | :  |||
Db         64 RLKNMTSIYLLNLAISDLLFLFTLPFWIDYKLKDDWVFGDAMCKILSGFYYTGLYSEIFF 123

Qy        131 IILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVC 190
              ||||||||||||||||||:||||||||:||:| | :|: ||:||: |:| | | : : |
Db        124 IILLTIDRYLAIVHAVFALRARTVTFGVITSIIIWALAILASMPGLYFSKTQWEFTHHTC 183

Qy        191 GPYFP----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIF 246
                :||    | |  |  :  |: |||||||:|:|||:||:| |||  ||||  :|||:||
Db        184 SLHFPHESLREWKLFQALKLNLFGLVLPLLVMIICYTGIIKILLRRPNEKK-SKAVRLIF 242

Qy        247 TIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYA 306
              |||::|||||||||: ||:: ||:|     || :  || | |||| :  ||||:||:|||
Db        243 VIMIIFFLFWTPYNLTILISVFQDFLFTHECEQSRHLDLAVQVTEVIAYTHCCVNPVIYA 302

Qy        307 FVGEKF----RSLFH 317
              ||||:|    | |||
Db        303 FVGERFRKYLRQLFH 317
```

RESULT 5
I49341
MIP-1 alpha receptor like-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49341
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta
chemokine receptor-like genes, including the gene for a functional macrophage
inflammatory protein-1 alpha receptor.
A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49341
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-359 <RES>
A;Cross-references: UNIPROT:Q8K3M7; EMBL:U28406; NID:g881551; PID:g881552
C;Superfamily: vertebrate rhodopsin

Query Match 48.7%; Score 960; DB 2; Length 359;
Best Local Similarity 50.1%; Pred. No. 2.2e-76;
Matches 187; Conservative 59; Mismatches 89; Indels 38; Gaps 7;

```
Qy         10 IRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILIN 69
              |:   || |  || ::|::  || |  :|::|: |||||||||| | :|||:||||||
Db          8 IKTVVESFE--TTPYEYEWAPPCEKVRIKELGSWLLPPLYSLVFIIGLLGNMMVVLILIK 65

Qy         70 CKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAA-NEWVFGNAMCKLFTGLYHIGYFGGI 128
               :||: :|:||| |||||||||| |:| | |    ||| ||: |||: :| |::  :  |
Db         66 YRKLQIMTNIYLFNLAISDLLFLFTVPFWIHYVLWNEWGFGHYMCKMLSGFYYLALYSEI 125

Qy        129 FFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVY 188
              |||||||||||||||||||||:||||||  :||:||| :|  |::|  || : |     :
Db        126 FFIILLTIDRYLAIVHAVFALRARTVTFATITSIITWGLAGLAALPEFIFHESQDSFGEF 185

Qy        189 VCGPYFPRG----WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRV 244
               | | :| |    |  || :  || || ||||:||||||||:|||||| | ||:|:|:|:
Db        186 SCSPRYPEGEEDSWKRFHALRMNIFGLALPLLVMVICYSGIIKTLLRCPN-KKKHKAIRL 244

Qy        245 IFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPII 304
              || :|||:|:||||||:|:| : |   |  ::|| :  || | |||| :  ||||:||:|
Db        245 IFVVMIVFFIFWTPYNLVLLFSAFHSTFLETSCEQSKHLDLAMQVTEVIAYTHCCVNPVI 304

Qy        305 YAFVGEKFRS----LFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGL---LDGRGKG 357
              ||||||:||      ||                        :||: | : :   | |   |
Db        305 YAFVGERFRKHLRLFFH----------------------RNVQFTWENIFQFLPGEENG 341

Qy        358 KSIGRAPEASLQD 370
              ::   :|    |:
Db        342 RTSSVSPSTGEQE 354
```

RESULT 6
I49339
macrophage inflammatory protein-1 alpha receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49339
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.
A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49339
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <RES>
A;Cross-references: UNIPROT:P51675; EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
C;Superfamily: vertebrate rhodopsin

```
  Query Match             45.8%;  Score 902.5;  DB 2;  Length 355;
  Best Local Similarity   53.1%;  Pred. No. 2.4e-71;
  Matches  170;  Conservative   58;  Mismatches   75;  Indels   17;  Gaps    6;

Qy         21 TTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIY 80
              || |||    || |  |:  || |||||||||| | |||:||:|:|:  ::|: :| ||
Db         13 TTEFDYGDSTPCQKTAVRAFGAGLLPPLYSLVFIIGVVGNVLVILVLMQHRRLQSMTSIY 72

Qy         81 LLNLAISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRY 139
              | |||:|||:|| ||| |  :   ::|:||:||||| :| |::| :  ||||||||||
Db         73 LFNLAVSDLVFLFTLPFWIDYKLKDDWIFGDAMCKLLSGFYYLGLYSEIFFIILLTIDRY 132

Qy        140 LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP---- 195
              |||||||||:|||||  |::||:||| :|: ||:| : | | | | :   | |:||
Db        133 LAIVHAVFALRARTVTLGIITSIITWALAILASMPALYFFKAQWEFTHRTCSPHFPYKSL 192

Qy        196 RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLF 255
              : |  |  :  |:|||:||||:|:|||:||:: |||  |  :|: :|||:|| | :::||
Db        193 KQWKRFQALKLNLLGLILPLLVMIICYAGIIRILLR-RPSEKKVKAVRLIFAITLLFFLL 251

Qy        256 WTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF--- 312
              |||||: : :: ||:    : || :  || | |||| :  ||||:||||| ||||:|
Db        252 WTPYNLSVFVSAFQDVLFTNQCEQSKHLDLAMQVTEVIAYTHCCVNPIIYVFVGERFWKY 311

Qy        313 -RSLF--HIALGCRIAPLQK 329
               | ||  |:|:     || |
Db        312 LRQLFQRHVAI-----PLAK 326


RESULT 7
G02436
chemokine (C-C) receptor 3 - human
N;Alternate names: C-C CKR-3
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02436; A57237
R;Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A;Reference number: H01272
A;Accession: G02436
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <PON>
A;Cross-references: UNIPROT:P51677; EMBL:U49727; NID:g1477560; PIDN:AAB09726.1;
PID:g1477561
R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A;Title: Cloning and functional expression of a human eosinophil CC chemokine
receptor.
A;Reference number: A57237; MUID:95348056; PMID:7622448
A;Accession: A57237
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-106,'N',108-275,'S',277-280,'R',282-355 <COM>
A;Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580
```

A;Note: the translated sequence in GenBank entry HSU28694, release 113.0,
PIDN:AAC50469.1, differs from the published sequence in having 281-Leu
C;Genetics:
A;Gene: GDB:CMKBR3
A;Cross-references: GDB:579624; OMIM:601268
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein;
transmembrane protein
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-261/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status
predicted

  Query Match 45.2%; Score 890.5; DB 2; Length 355;
  Best Local Similarity 54.6%; Pred. No. 2.7e-70;
  Matches 167; Conservative 56; Mismatches 72; Indels 11; Gaps 5;

```
Qy         21 TTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIY 80
              |:::| | |  | | | : : || :|||||||  | :||::||:|||  ::|: :|:||
Db         14 TSYYD-DVGLLCEKADTRALMAQFVPPLYSLVFTVGLLGNVVVVMILIKYRRLRIMTNIY 72

Qy         81 LLNLAISDLLFLITLPLWAHSA-ANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRY 139
              |||||||||||||:||| | |    : ||||: |||| :| || | :  ||||||||||||
Db         73 LLNLAISDLLFLVTLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRY 132

Qy        140 LAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR--- 196
              ||||||||||:||||||||:||::|| :|| |::|  || : ::     :|   :|
Db        133 LAIVHAVFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEETLCSALYPEDTV 192

Qy        197 -GWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLF 255
               | :|||:   |  ||||||:| |||:||:|||||| : ||:::|:|:|| || |:|:|
Db        193 YSWRHFHTLRMTIFCLVLPLLVMAICYTGIIKTLLRCPS-KKKYKAIRLIFVIMAVFFIF 251

Qy        256 WTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS- 314
              |||||: |||:::|     ::|| |  ||    ||| :  :|||:||:|||||||:||
Db        252 WTPYNVAILLSSYQSILFGNDCERTKHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKY 311

Qy        315 ---LFH 317
                 ||
Db        312 LRHFFH 317
```

RESULT 8
JC4587
chemokine (C-C) receptor 4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: JC4587
R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996

A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human CC CKR-4.
A;Reference number: JC4587; MUID:96136324; PMID:8573157
A;Accession: JC4587
A;Molecule type: mRNA
A;Residues: 1-360 <HOO>
A;Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

  Query Match 42.3%; Score 833; DB 2; Length 360;
  Best Local Similarity 47.9%; Pred. No. 2.9e-65;
  Matches 160; Conservative 63; Mismatches 89; Indels 22; Gaps 5;

```
Qy         10 IRNTNESGEEVTTFFDYD-YGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILI 68
              : :| :      ::: |:    || |  :|  |   |||||||||: |  || :|||:|
Db          6 VTDTTQDETVYNSYYFYESMPKPCTKEGIKAFGEVFLPPLYSLVFLLGLFGNSVVVLVLF 65

Qy         69 NCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGI 128
               |:|| :||:|||||||||||||:::|| | : ||::||||  :||: : :| :|:: ||
Db         66 KYKRLKSMTDVYLLNLAISDLLFVLSLPFWGYYAADQWVFGLGLCKIVSWMYLVGFYSGI 125

Qy        129 FFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVY 188
              |||:|::|||||||||||||:|||||:|:||:||:||| ||||||:||::|: |  | :
Db        126 FFIMLMSIDRYLAIVHAVFSLKARTLTYGVITSLITWSVAVFASLPGLLFSTCYTEHNHT 185

Qy        189 VCGPYF---PRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVI 245
               |   :      |    ::  |:|||::|| ||:  || |::||  |:|||| :||||:|
Db        186 YCKTQYSVNSTTWKVLSSLEINVLGLLIPLGIMLFWYSMIIRTLQHCKNEKK-NRAVRMI 244

Qy        246 FTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIY 305
              | :::::  ||||||:|: | |  |   | :|     || | | |||||  |||:||:||
Db        245 FGVVVLFLGFWTPYNVVLFLETLVELEVLQDCTLERYLDYAIQATETLGFIHCCLNPVIY 304

Qy        306 AFVGEKFR----SLFHIALGCRIAPLQKPVCGGP 335
               |:|||||     ||               | ||
Db        305 FFLGEKFRKYITQLFR-------------TCRGP 325
```

RESULT 9
A57160
chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57160

R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Wells, T.N.C.
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line.
A;Reference number: A57160; MUID:95370289; PMID:7642634
A;Accession: A57160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: UNIPROT:P51679; GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A;Note: source clone K5-5
C;Genetics:
A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;40-65/Domain: transmembrane #status predicted <TM1>
F;76-97/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;151-175/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;29-276,110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 42.2%; Score 831.5; DB 2; Length 360;
Best Local Similarity 51.9%; Pred. No. 3.9e-65;
Matches 154; Conservative 58; Mismatches 80; Indels 5; Gaps 3;

```
Qy         31 PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAISDLL 90
              ||  |  :|  |   |||||||||:|| :|| :|||:|   |:|: :||:|||||||||||
Db         28 PCTKEGIKAFGELFLPPLYSLVFVFGLLGNSVVVLVLFKYKRLRSMTDVYLLNLAISDLL 87

Qy         91 FLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVHAVFALK 150
              |: :|| | : ||::|||| :||: : :| :|:: ||||::|::||||||||||||:|:
Db         88 FVFSLPFWGYYAADQWVFGLGLCKMISWMYLVGFYSGIFFVMLMSIDRYLAIVHAVFSLR 147

Qy        151 ARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---WNNFHTIMRN 207
              |||:|:||:||: || ||||||:|| :|: |  | :   |   :      |    ::  |
Db        148 ARTLTYGVITSLATWSVAVFASLPGFLFSTCYTERNHTYCKTKYSLNSTTWKVLSSLEIN 207

Qy        208 ILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTPYNIVILLNT 267
              |||||:|| ||: ||| |::||  |:|||| ::||::|| :::::  ||||||||: | |
Db        208 ILGLVIPLGIMLFCYSMIIRTLQHCKNEKK-NKAVKMIFAVVVLFLGFWTPYNIVLFLET 266

Qy        268 FQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS-LFHIALGCR 323
```

```
                |   | :|     || | | ||||   |||:|||||  |:|||||  :  :   ||
Db        267 LVELEVLQDCTFERYLDYAIQATETLAFVHCCLNPIIYFFLGEKFRKYILQLFKTCR 323


RESULT 10
S55594
G protein-coupled receptor E1 - equine herpesvirus 2
C;Species: equine herpesvirus 2
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S55594
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
A;Accession: S55594
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-383 <TEL>
A;Cross-references: UNIPROT:Q89609; GB:U20824; NID:g695172; PIDN:AAC13788.1;
PID:g695173
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

  Query Match             40.3%;  Score 794.5;  DB 2;  Length 383;
  Best Local Similarity   44.3%;  Pred. No. 7.2e-62;
  Matches  164;  Conservative   60;  Mismatches  107;  Indels   39;  Gaps    7;

Qy          4 TSRSRFIRNTNESGEEVTTFFDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNM 61
              |: :  : :|| | :      | ||   |||:| |  :: ||::| || |||:|| :||:
Db         32 TTIASLVPSTNSSEDYYDDLDDVDYEESAPCYKSDTTRLAAQVVPALYLLVFLFGLLGNI 91

Qy         62 LVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAH--SAANEWVFGNAMCKLFTGL 119
              |||:|:|   |:| ||:: ||||||||||||:||| | |     ::| || ::|||  |:
Db         92 LVVIIVIRYMKIKNLTNMLLLNLAISDLLFLLTLPFWMHYIGMYHDWTFGISLCKLLRGV 151

Qy        120 YHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFT 179
               ::  :  :| |||||:|||||:|:|| ||: |||| |:|| | || :|   |:|   |
Db        152 CYMSLYSQVFCIILLTVDRYLAVVYAVTALRFRTVTCGIVTCVCTWFLAGLLSLPEFFFH 211

Qy        180 KCQKEDSVYVCGPYFP----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNE 235
              | ::    | ||:|      |   |     :| |:|||||| :||  |:: ||| |
Db        212 GHQDDNGRVQCDPYYPEMSTNVWRRAHVAKVIMLSLILPLLIMAVCYYVIIRRLLR-RPS 270

Qy        236 KKRHRAVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGM 295
              ||:::|:|:|| ||: ||:|||||||:|||:||        |  :| || |  :|:|:
Db        271 KKKYKAIRLIFVIMVAYFVFWTPYNIVLLLSTFHATLLNLQCALSSNLDMALLITKTVAY 330

Qy        296 THCCINPIIYAFVGEKFR----SLFHIALG---CRIAPLQKPVCGGPGVRPGKNVKVTTQ 348
              |||||||:||||||||||      ||  :    |:  |
Db        331 THCCINPVIYAFVGEKFRRHLYHFFHTYVAIYLCKYIP---------------------- 368

Qy        349 GLLDGRGKGK 358
              | | |:||
Db        369 -FLSGDGEGK 377


RESULT 11
```

I49340
MIP-1 alpha receptor like-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49340
R;Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.
A;Reference number: I49339; MUID:95340546; PMID:7542241
A;Accession: I49340
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-356 <RES>
A;Cross-references: UNIPROT:P51676; EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
C;Superfamily: vertebrate rhodopsin

  Query Match 37.1%; Score 731; DB 2; Length 356;
  Best Local Similarity 46.6%; Pred. No. 2.4e-56;
  Matches 137; Conservative 59; Mismatches 92; Indels 6; Gaps 3;

```
Qy         25 DYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNL 84
              |:  |  |   :|:  |  :  |||||||| | :|::||||:||  |:|: :| ||| ||
Db         18 DFMSGFLCFSINVRAFGITVPTPLYSLVFIIGVIGHVLVVLVLIQHKRLRNMTSIYLFNL 77

Qy         85 AISDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIV 143
              |||||:|| ||| |  :    :|:|||||||  :| |::| :  :||| |||||||||:|
Db         78 AISDLVFLSTLPFWVDYIMKGDWIFGNAMCKFVSGFYYLGLYSDMFFITLLTIDRYLAVV 137

Qy        144 HAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR----GWN 199
              | ||||:|||||||:::|:|||::|   |:| :   | | | : : |    ||     :
Db        138 HVVFALRARTVTFGIISSIITWVLAALVSIPCLYVFKSQMEFTYHTCRAILPRKSLIRFL 197

Qy        200 NFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTPY 259
               |  :  |||||:|||| |:|||: |:  | | |  ||: : :|:|| | :::||   ||
Db        198 RFQALTMNILGLILPLLAMIICYTRIINVLHR-RPNKKKAKVMRLIFVITLLFFLLLAPY 256

Qy        260 NIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFR 313
               :   :: |::     :|  : |:| : . :|| |  ||||:||:|| |||::||
Db        257 YLAAFVSAFEDVLFTPSCLRSQQVDLSLMITEALAYTHCCVNPVIYVFVGKRFR 310
```

RESULT 12
JC5067
G protein-coupled receptor CKR-L1 - human
N;Alternate names: chemokine receptor-like protein TER1; GPR-CY6
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5067; G02776; G02387
R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like genes.
A;Reference number: JC5067; MUID:97040707; PMID:8886020
A;Accession: JC5067

A;Molecule type: DNA
A;Residues: 1-355 <ZAB>
A;Cross-references: UNIPROT:P51685; EMBL:Z79782; NID:g1668735; PIDN:CAB02142.1;
PID:g1668736
R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.;
Santoni, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: H01714
A;Accession: G02776
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <NAP>
A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979
R;Bonner, T.I.
submitted to the EMBL Data Library, January 1996
A;Reference number: H01154
A;Accession: G02387
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <BON>
A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057
C;Comment: This protein belongs to the family of beta chemokine receptors.
C;Genetics:
A;Gene: GDB:CMKBR8; CMKBRL2; TER1; CKR-L1
A;Cross-references: GDB:6053733; OMIM:601834
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;36-63/Domain: transmembrane #status predicted <TM1>
F;73-94/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;200-222/Domain: transmembrane #status predicted <TM5>
F;239-260/Domain: transmembrane #status predicted <TM6>
F;281-304/Domain: transmembrane #status predicted <TM7>

  Query Match 36.7%; Score 723; DB 2; Length 355;
  Best Local Similarity 43.5%; Pred. No. 1.2e-55;
  Matches 131; Conservative 59; Mismatches 103; Indels 8; Gaps 3;

```
Qy         20 VTTFFDYDY----GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC 75
              |||  || |     :||    ::  |  ||   | |:|:|  :|| ||:|:|: ||||:
Db          9 VTTVTDYYYPDIFSSPCDAELIQTNGKLLLAVFYCLLFVFSLLGNSLVILVLVVCKKLRS 68

Qy         76 LTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLT 135
              :||:||||||:|||||: : |   :   ::||||  |||: :| |:||::  :||| |::
Db         69 ITDVYLLNLALSDLLFVFSFPFQTYYLLDQWVFGTVMCKVVSGFYYIGFYSSMFFITLMS 128

Qy        136 IDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP 195
              :|||||:||||:||| ||:  |    :  || |: |::| ::| :   || |  |  ::
Db        129 VDRYLAVVHAVYALKVRTIRMGTTLCLAVWLTAIMATIPLLVFYQVASEDGVLQCYSFYN 188

Qy        196 R---GWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVY 252
              :    |  |     |||||::|  | : ||  ||  | ||:|  |  :|:|::  ::|
Db        189 QQTLKWKIFTNFKMNILGLLIPFTIFMFCYIKILHQLKRCQNHNKT-KAIRLVLIVVIAS 247

Qy        253 FLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF 312
```

```
                ||| |:|:|: | :      |  |  : ||  || ||| :  ||||:||:||||||||
Db        248 LLFWVPFNVVLFLTSLHSMHILDGCSISQQLTYATHVTEIISFTHCCVNPVIYAFVGEKF 307

Qy        313 R 313
              :
Db        308 K 308
```

RESULT 13
I58186
probable G protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I58186
R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and brain related to chemokine receptors.
A;Reference number: I58186; MUID:94323113; PMID:8047298
A;Accession: I58186
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-354 <RES>
A;Cross-references: UNIPROT:P35411; EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

  Query Match   35.8%; Score 704.5; DB 2; Length 354;
  Best Local Similarity   47.6%; Pred. No. 5e-54;
  Matches 151; Conservative   43; Mismatches 112; Indels   11; Gaps   6;

```
Qy         24 FDYDYGA-PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLL 82
              |:||  |  |:  |:   |   |   ||||| || |||:|||| | | :| | :||||||
Db         13 FEYDDSAEACYLGDIVAFGTIFLSIFYSLVFTFGLVGNLLVVLALTNSRKSKSITDIYLL 72

Qy         83 NLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAI 142
              |||:|||||: ||| | |   :     |||||| |  : ||:||||||| :::|||||||
Db         73 NLALSDLLFVATLPFWTHYLISHEGLHNAMCKLTTAFFFIGFFGGIFFITVISIDRYLAI 132

Qy        143 VHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRGWNNFH 202
              | |  ::  |||  ||  |:  |  |:  : |  :||| :|::    |   :|
Db        133 VLAANSMNNRTVQHGVTISLGVWAAAILVASPQFMFTK-RKDNE---CLGDYPEVLQEIW 188

Qy        203 TIMR----NILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTP 258
               ::|    |||| |||||||  ||  |::||  |:| ||  ||:|:|  :::|:||||||
Db        189 PVLRNSEVNILGFVLPLLIMSFCYFRIVRTLFSCKNRKKA-RAIRLILLVVVVFFLFWTP 247

Qy        259 YNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS-LFH 317
              |||||  | | : :    :|     |  |  ||||:  :|||:|| |||| |||||  | |
Db        248 YNIVIFLETLKFYNFFPSCGMKRDLRWALSVTETVAFSHCCLNPFIYAFAGEKFRRYLRH 307

Qy        318 IALGCRIAPLQKPVCGG 334
              :   |      :||  |
Db        308 LYNKCLAVLCGRPVHAG 324
```

RESULT 14
JC4304
orphan G protein-coupled receptor - human
N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4304
R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to genes for chemokine receptors and is expressed in lymphoid and neuraltissues.
A;Reference number: JC4304; MUID:96011651; PMID:7590284
A;Accession: JC4304
A;Molecule type: mRNA
A;Residues: 1-355 <RAP>
A;Cross-references: UNIPROT:P49238; GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals and transduces those signals into an intracellular response.
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and interacts between the nervous and immune systems.
C;Genetics:
A;Gene: v28
A;Map position: 3pter-p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F;35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;275-296/Domain: transmembrane #status predicted <TM7>

Query Match 35.4%; Score 698; DB 2; Length 355;
Best Local Similarity 45.3%; Pred. No. 1.9e-53;
Matches 146; Conservative 49; Mismatches 111; Indels 16; Gaps 7;

```
Qy         18 EEVTTFFDY-DYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCL 76
              | ||  |:| |    |:  |:   |   |   ||::|  | |||:|||  | | || | :
Db          6 ESVTENFEYDDLAEACYIGDIVVFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSV 65

Qy         77 TDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTI 136
              |||||||||:|||||: ||| | |   ||    |||||  |  : ||:|| |||| :::|
Db         66 TDIYLLNLALSDLLFVATLPFWTHYLINEKGLHNAMCKFTTAFFFIGFFGSIFFITVISI 125

Qy        137 DRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPR 196
              ||||||| |  ::  |||  ||  |:  |  |:  : |  :||| |||:    |   :|
Db        126 DRYLAIVLAANSMNNRTVQHGVTISLGVWAAAILVAAPQFMFTK-QKENE---CLGDYPE 181

Qy        197 GWNNFHTIMRNI----LGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVY 252
                    ::||:    || :|||||  ||  |::||  |:| ||  :|:::|  ::||:
Db        182 VLQEIWPVLRNVETNFLGFLLPLLIMSYCYFRIIQTLFSCKNHKKA-KAIKLILLVVIVF 240
```

```
Qy        253 FLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKF 312
              ||||||||::| | | : :    :|:    |  |  ||||:  :|||:||:|||| ||||
Db        241 FLFWTPYNVMIFLETLKLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKF 300

Qy        313 RS-LFHIALGCRIAPLQKPVCG 333
              |  |:|:   |        :||
Db        301 RRYLYHLYGKCLAV-----LCG 317
```

RESULT 15
JC5942
chemokine receptor - human
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: JC5942
R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A;Title: Cloning and characterization of a novel human chemokine receptor.
A;Reference number: JC5942; MUID:98139902; PMID:9473515
A;Accession: JC5942
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-344 <FAN>
A;Cross-references: UNIPROT:O00421; GB:U97123; NID:g2897070; PIDN:AAC39595.1;
PID:g2897071
C;Superfamily: vertebrate rhodopsin

  Query Match   32.7%; Score 644.5; DB 2; Length 344;
  Best Local Similarity   39.9%; Pred. No. 8.7e-49;
  Matches 132; Conservative   58; Mismatches 120; Indels   21; Gaps   6;

```
Qy         27 DYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAI 86
              |    | |:| : : |||:| | | ||: | : |:|||||:  | || : :|||||||:
Db         23 DEAEQCDKYDAQALSAQLVPSLCSAVFVIGVLDNLLVVLILVKYKGLKRVENIYLLNLAV 82

Qy         87 SDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVH-A 145
              |:| ||:||| |||:       |: |||:  ||| :| :   ||  |||: |||  :|
Db         83 SNLCFLLTLPFWAHAG------GDPMCKILIGLYFVGLYSETFFNCLLTVQRYLVFLHKG 136

Qy        146 VFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCG----PYFPRG---W 198
              |    | |  |::|||: |: |: |::|  :  | | ||  | |     |: |     |
Db        137 NFFSARRRVPCGIITSVLAWVTAILATLPEYVVYKPQMEDQKYKCAFSRTPFLPADETFW 196

Qy        199 NNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTP 258
              :| |:  ||  ||||| |    | : |||   |  ::|:   :::| ||:|: | | |
Db        197 KHFLTLKMNISVLVLPLFIFTFLYVQMRKTL---RFREQRYSLFKLVFAIMVVFLLMWAP 253

Qy        259 YNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRS---- 314
              |||   |:||:| | ||:|:|:  ||::  :|: :  |||||||::|||:   |
Db        254 YNIAFFLSTFKEHFSLSDCKSSYNLDKSVHITKLIATTHCCINPLLYAFLDGTFSKYLCR 313

Qy        315 LFHIALGCRIAPLQKPVCGGPGVRPGKNVKV 345
              ||:    : |  :   |     |  : :|
Db        314 CFHLRSNTPLQPRGQSAQGTSREEPDHSTEV 344
```

Search completed: March 31, 2005, 14:07:49

Job time : 47 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 31, 2005, 14:00:55 ; Search time 147 Seconds
(without alignments)
843.644 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 1970
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
1	1970	100.0	374	10	US-09-893-512-13	Sequence 13, Appl
2	1970	100.0	374	14	US-10-039-659-14	Sequence 14, Appl
3	1970	100.0	374	14	US-10-239-423-63	Sequence 63, Appl
4	1970	100.0	374	16	US-10-754-071-14	Sequence 14, Appl
5	1970	100.0	374	16	US-10-741-601-287	Sequence 287, App
6	1823	92.5	344	9	US-09-779-879A-9	Sequence 9, Appli
7	1823	92.5	344	9	US-09-779-880A-9	Sequence 9, Appli
8	1823	92.5	344	14	US-10-232-686-9	Sequence 9, Appli
9	1823	92.5	344	14	US-10-067-800-9	Sequence 9, Appli
10	1823	92.5	344	14	US-10-135-839-9	Sequence 9, Appli
11	1727.5	87.7	329	9	US-09-725-285-9	Sequence 9, Appli
12	1727.5	87.7	329	9	US-09-195-662A-9	Sequence 9, Appli
13	1727.5	87.7	329	9	US-09-339-912A-9	Sequence 9, Appli
14	1727.5	87.7	329	9	US-09-502-783A-9	Sequence 9, Appli
15	1727.5	87.7	329	16	US-10-791-905-9	Sequence 9, Appli
16	1651.5	83.8	360	9	US-09-131-827A-2	Sequence 2, Appli
17	1651.5	83.8	360	14	US-10-225-567A-460	Sequence 460, App
18	1651.5	83.8	360	14	US-10-164-649-50	Sequence 50, Appl
19	1651.5	83.8	360	14	US-10-239-423-64	Sequence 64, Appl
20	1651.5	83.8	360	14	US-10-439-845-8	Sequence 8, Appli
21	1651.5	83.8	360	16	US-10-741-601-285	Sequence 285, App
22	1651.5	83.8	360	16	US-10-741-601-286	Sequence 286, App
23	1650.5	83.8	360	9	US-09-131-827A-20	Sequence 20, Appl
24	1645.5	83.5	360	9	US-09-938-719-7	Sequence 7, Appli
25	1645.5	83.5	360	9	US-09-939-226-7	Sequence 7, Appli
26	1645.5	83.5	360	9	US-09-938-703-7	Sequence 7, Appli
27	1645.5	83.5	360	10	US-09-826-509-473	Sequence 473, App
28	1645.5	83.5	360	16	US-10-661-798-7	Sequence 7, Appli
29	1645.5	83.5	360	16	US-10-612-791-7	Sequence 7, Appli
30	1645.5	83.5	360	17	US-10-925-095-473	Sequence 473, App
31	1614.5	82.0	360	14	US-10-164-649-51	Sequence 51, Appl
32	1589.5	80.7	347	9	US-09-104-792-3	Sequence 3, Appli
33	1589.5	80.7	347	14	US-10-176-078-3	Sequence 3, Appli
34	1582.5	80.3	384	10	US-09-893-512-14	Sequence 14, Appl
35	1236	62.7	352	14	US-10-151-274-5	Sequence 5, Appli
36	1230	62.4	352	14	US-10-164-649-52	Sequence 52, Appl
37	1224	62.1	352	9	US-09-725-285-2	Sequence 2, Appli
38	1224	62.1	352	9	US-09-759-841-2	Sequence 2, Appli
39	1224	62.1	352	9	US-09-779-879A-22	Sequence 22, Appl
40	1224	62.1	352	9	US-09-779-880A-22	Sequence 22, Appl
41	1224	62.1	352	9	US-09-813-653-15	Sequence 15, Appl
42	1224	62.1	352	9	US-09-796-202-1	Sequence 1, Appli
43	1224	62.1	352	9	US-09-195-662A-2	Sequence 2, Appli
44	1224	62.1	352	9	US-09-339-912A-2	Sequence 2, Appli
45	1224	62.1	352	9	US-09-938-719-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-893-512-13
; Sequence 13, Application US/09893512
; Publication No. US20030017530A1

; GENERAL INFORMATION:
; APPLICANT: OWMAN, CHRISTER
; TITLE OF INVENTION: HEPTAHELIX RECEPTOR AND ITS USE AS LEUKOTRIENE B4
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 07675.0001-03 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/09/893,512
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/061,789
; PRIOR FILING DATE: 1997-10-14
; PRIOR APPLICATION NUMBER: 60/081,958
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 09/170,069
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-512-13

Query Match 100.0%; Score 1970; DB 10; Length 374;
Best Local Similarity 100.0%; Pred. No. 2.8e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374
```

RESULT 2
US-10-039-659-14
; Sequence 14, Application US/10039659

```
; Publication No. US20030018167A1
;   GENERAL INFORMATION:
;        APPLICANT: Wang, Wei
;                   Gish, Kurt C.
;                   Schall, Thomas J.
;                   Vicari, Alain P.
;                   Zlotnik, Albert
;        TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DNAX Research Institute
;             STREET: 901 California Avenue
;             CITY: Palo Alto
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94304-1104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/039,659
;             FILING DATE: 03-Jan-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/887,977
;             FILING DATE: 03-JUL-1997
;             APPLICATION NUMBER: US 60/021,644
;             FILING DATE: 05-JUL-1996
;             APPLICATION NUMBER: US 60/028,329
;             FILING DATE: 11-OCT-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ching, Edwin P.
;             REGISTRATION NUMBER: 34,090
;             REFERENCE/DOCKET NUMBER: DX0589K1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-852-9192
;             TELEFAX: 650-496-1200
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 374 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-039-659-14

  Query Match             100.0%;  Score 1970;  DB 14;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-163;
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
```

```
Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374
```

RESULT 3
US-10-239-423-63
; Sequence 63, Application US/10239423
; Publication No. US20030186889A1
; GENERAL INFORMATION:
; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells
and
; TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand
Interaction
; FILE REFERENCE: 022217us
; CURRENT APPLICATION NUMBER: US/10/239,423
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: DE10016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-63

Query Match 100.0%; Score 1970; DB 14; Length 374;
Best Local Similarity 100.0%; Pred. No. 2.8e-163;

```
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374


RESULT 4
US-10-754-071-14
; Sequence 14, Application US/10754071
; Publication No. US20040137578A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Wei
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Schall, Thomas J.
;  APPLICANT:  Vicari, Alain P.
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: Chemokine TECK Polypeptides
;  FILE REFERENCE: DX0589K1C US
;  CURRENT APPLICATION NUMBER: US/10/754,071
;  CURRENT FILING DATE:  2004-01-07
;  PRIOR APPLICATION NUMBER: US 10/039,659
;  PRIOR FILING DATE: 2002-01-03
;  PRIOR APPLICATION NUMBER: US 08/887,977
;  PRIOR FILING DATE: 1997-07-03
;  PRIOR APPLICATION NUMBER: US 60/021,664
;  PRIOR FILING DATE: 1996-07-05
;  PRIOR APPLICATION NUMBER: US 60/028,329
;  PRIOR FILING DATE: 1996-10-11
;  PRIOR APPLICATION NUMBER: US 60/048,593
;  PRIOR FILING DATE: 1997-06-04
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
```

; SEQ ID NO 14
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-754-071-14

Query Match 100.0%; Score 1970; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 2.8e-163;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374
```

RESULT 5
US-10-741-601-287
; Sequence 287, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 287
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-287

```
  Query Match             100.0%;  Score 1970;  DB 16;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-163;
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374
```

```
RESULT 6
US-09-779-879A-9
; Sequence 9, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen, Craig A.
;  APPLICANT:  Roschke, Viktor
;  APPLICANT:  Li, Yi
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
;  FILE REFERENCE: 1488.115000A
;  CURRENT APPLICATION NUMBER: US/09/779,879A
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: US 60/181,258
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 60/187,999
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: US 60/234,336
;  PRIOR FILING DATE: 2000-09-22
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 344
```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-9

  Query Match 92.5%; Score 1823; DB 9; Length 344;
  Best Local Similarity 100.0%; Pred. No. 1.7e-150;
  Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||
Db        301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
```

RESULT 7
US-09-779-880A-9
; Sequence 9, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 344
;   TYPE: PRT

; ORGANISM: Homo sapiens
US-09-779-880A-9

  Query Match 92.5%; Score 1823; DB 9; Length 344;
  Best Local Similarity 100.0%; Pred. No. 1.7e-150;
  Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
               |||||||||||||||||||||||||||||||||||||||||||
Db        301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
```

RESULT 8
US-10-232-686-9
; Sequence 9, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 344
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-232-686-9

```
  Query Match             92.5%;  Score 1823;  DB 14;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-150;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy          78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy         138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy         198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy         258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy         318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
               |||||||||||||||||||||||||||||||||||||||||||
Db         301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
```

```
RESULT 9
US-10-067-800-9
; Sequence 9, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
;  APPLICANT: Roschke, Viktor
;  APPLICANT:  Rosen, Craig A.
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
;  FILE REFERENCE: 1488.115000I
;  CURRENT APPLICATION NUMBER: US/10/067,800
;  CURRENT FILING DATE:  2002-02-08
;  PRIOR APPLICATION NUMBER: PCT/US01/04153
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 09/779,880
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/297,257
;  PRIOR FILING DATE: 2001-06-12
;  PRIOR APPLICATION NUMBER: 60/310,458
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: 60/328,447
;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: 60/341,725
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 344
```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-9

  Query Match 92.5%; Score 1823; DB 14; Length 344;
  Best Local Similarity 100.0%; Pred. No. 1.7e-150;
  Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy          78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy         138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy         198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy         258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy         318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
               |||||||||||||||||||||||||||||||||||||||||||
Db         301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344
```

RESULT 10
US-10-135-839-9
; Sequence 9, Application US/10135839
; Publication No. US20030166024A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 344
;   TYPE: PRT

```
;   ORGANISM: Homo sapiens
US-10-135-839-9

  Query Match             92.5%;  Score 1823;  DB 14;  Length 344;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-150;
  Matches  344;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 120

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 180

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 240

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 300

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||
Db        301 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 344


RESULT 11
US-09-725-285-9
; Sequence 9, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
;  APPLICANT:   Li, Yi
;  APPLICANT:  Ruben, Steven, M.
;  TITLE OF INVENTION:   Antibodies to Human G-Protein Chemokine Receptor
HDGNR10
;  TITLE OF INVENTION:  (CCR5 Receptor)
;  FILE REFERENCE:   1488.1150003
;  CURRENT APPLICATION NUMBER: US/09/725,285
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER:   09/339,912
;  PRIOR FILING DATE:   1999-06-25
;  PRIOR APPLICATION NUMBER:   09/195,662
;  PRIOR FILING DATE:   1998-11-18
;  PRIOR APPLICATION NUMBER:   08/466,343
;  PRIOR FILING DATE:   1995-06-06
;  NUMBER OF SEQ ID NOS:   9
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Protein
```

US-09-725-285-9

```
  Query Match             87.7%;  Score 1727.5;  DB 9;  Length 329;
  Best Local Similarity   95.6%;  Pred. No. 3.3e-142;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels   15;  Gaps    1;

Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              |||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI--------------- 105

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||
Db        286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329
```

RESULT 12
US-09-195-662A-9
; Sequence 9, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-195-662A-9

```
  Query Match             87.7%;  Score 1727.5;  DB 9;  Length 329;
  Best Local Similarity   95.6%;  Pred. No. 3.3e-142;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels   15;  Gaps    1;
```

```
Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI---------------- 105

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||
Db        286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329
```

RESULT 13
US-09-339-912A-9
; Sequence 9, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-339-912A-9

Query Match 87.7%; Score 1727.5; DB 9; Length 329;
Best Local Similarity 95.6%; Pred. No. 3.3e-142;
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

```
Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60
```

```
Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              ||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI---------------- 105

Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||
Db        286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329
```

RESULT 14
US-09-502-783A-9
; Sequence 9, Application US/09502783A
; Patent No. US20020132269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)
; TITLE OF INVENTION: HDGNR10
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-502-783A-9

Query Match 87.7%; Score 1727.5; DB 9; Length 329;
Best Local Similarity 95.6%; Pred. No. 3.3e-142;
Matches 329; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

```
Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              ||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI---------------- 105
```

```
Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||
Db        286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329
```

RESULT 15
US-10-791-905-9
; Sequence 9, Application US/10791905
; Publication No. US20040151719A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000P
; CURRENT APPLICATION NUMBER: US/10/791,905
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 10/127,764
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 09/502,783
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-791-905-9

  Query Match   87.7%; Score 1727.5; DB 16; Length 329;
  Best Local Similarity   95.6%; Pred. No. 3.3e-142;
  Matches 329; Conservative   0; Mismatches   0; Indels   15; Gaps   1;

```
Qy         18 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 77
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLT 60

Qy         78 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID 137
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 DIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHI---------------- 105
```

```
Qy        138 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 RYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG 165

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 225

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLFH 285

Qy        318 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 361
              |||||||||||||||||||||||||||||||||||||||||||
Db        286 IALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSIG 329
```

Search completed: March 31, 2005, 14:11:18
Job time : 156 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 31, 2005, 13:49:33 ; Search time 181 Seconds
(without alignments)
1058.108 Million cell updates/sec

Title: US-10-791-592-2
Perfect score: 1970
Sequence: 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1970	100.0	374	1	CKR2_HUMAN	P41597 homo sapien
2	1614.5	82.0	360	1	CKR2_MACMU	O18793 macaca mula
3	1346.5	68.4	373	1	CKR2_RAT	O55193 rattus norv
4	1332.5	67.6	373	1	CKR2_MOUSE	P51683 mus musculu
5	1327.5	67.4	373	2	Q6YT42	Q6yt42 sus scrofa
6	1252	63.6	352	2	Q95NC2	Q95nc2 callicebus
7	1247	63.3	354	2	Q68G28	Q68g28 rattus norv
8	1244	63.1	339	2	Q9TQT3	Q9tqt3 callithrix
9	1244	63.1	339	2	Q9TUV8	Q9tuv8 saguinus sp
10	1244	63.1	352	2	Q6WN98	Q6wn98 callithrix
11	1244	63.1	352	2	Q9MZA0	Q9mza0 callithrix
12	1244	63.1	354	1	CKR5_MOUSE	P51682 mus musculu
13	1243	63.1	339	2	Q9TQV5	Q9tqv5 saguinus sp
14	1243	63.1	352	2	Q95NC4	Q95nc4 ateles geof
15	1241	63.0	352	2	Q6WN93	Q6wn93 leontopithe

16	1241	63.0	352	2	Q6WN96	Q6wn96 leontopithe
17	1241	63.0	352	2	Q6WN97	Q6wn97 cebuella py
18	1240	62.9	339	2	Q9TUW0	Q9tuw0 saguinus sp
19	1239	62.9	352	2	Q6YT41	Q6yt41 sus scrofa
20	1239	62.9	352	2	Q9MZ99	Q9mz99 ateles sp.
21	1238.5	62.9	339	2	Q9TUV6	Q9tuv6 saguinus sp
22	1238	62.8	339	2	Q9TUW1	Q9tuw1 saguinus sp
23	1237	62.8	339	2	Q9TUV9	Q9tuv9 saguinus sp
24	1236	62.7	339	2	Q9TQW0	Q9tqw0 hylobates c
25	1236	62.7	352	1	CKR5_CERTO	O62743 cercocebus
26	1236	62.7	352	1	CKR5_HYLLE	O97883 hylobates l
27	1236	62.7	352	2	Q8HZT9	Q8hzt9 saimiri sci
28	1236	62.7	352	2	Q6WN92	Q6wn92 leontopithe
29	1236	62.7	352	2	Q6WN94	Q6wn94 leontopithe
30	1236	62.7	352	2	Q71RS2	Q71rs2 cercocebus
31	1235	62.7	339	2	Q9TSN3	Q9tsn3 macaca fasc
32	1235	62.7	352	2	O77776	O77776 cercocebus
33	1234	62.6	339	2	Q9TUV5	Q9tuv5 saguinus sp
34	1234	62.6	352	2	Q6WN95	Q6wn95 leontopithe
35	1233	62.6	339	2	Q9TUV2	Q9tuv2 alouatta ca
36	1233	62.6	352	2	Q95NE1	Q95ne1 cercocebus
37	1232	62.5	339	2	Q9TUT9	Q9tut9 macaca mula
38	1232	62.5	339	2	Q9TUV0	Q9tuv0 aotus trivi
39	1232	62.5	339	2	Q9TUV4	Q9tuv4 callithrix
40	1232	62.5	339	2	Q9TUX0	Q9tux0 hylobates c
41	1232	62.5	352	2	Q6WN91	Q6wn91 brachyteles
42	1231	62.5	339	2	Q9TUW9	Q9tuw9 hylobates c
43	1231	62.5	352	1	CKR5_HYLML	Q95nc0 hylobates m
44	1231	62.5	352	2	Q95NC9	Q95nc9 alouatta se
45	1231	62.5	352	2	Q9XT12	Q9xt12 cercopithec

ALIGNMENTS

```
RESULT 1
CKR2_HUMAN
ID   CKR2_HUMAN     STANDARD;      PRT;   374 AA.
AC   P41597;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
DE   (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
GN   Name=CCR2; Synonyms=CMKBR2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94195821; PubMed=8146186;
RA   Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,
RA   Coughlin S.R.;
RT   "Molecular cloning and functional expression of two monocyte
RT   chemoattractant protein 1 receptors reveals alternative splicing of
RT   the carboxyl-terminal tails.";
```

```
RL   Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94324942; PubMed=8048929;
RA   Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
RT   "cDNA cloning and functional expression of a human monocyte
RT   chemoattractant protein 1 receptor.";
RL   Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97150864; PubMed=8995400; DOI=10.1074/jbc.272.2.1038;
RA   Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;
RT   "Organization and differential expression of the human monocyte
RT   chemoattractant protein 1 receptor gene. Evidence for the role of the
RT   carboxyl-terminal tail in receptor trafficking.";
RL   J. Biol. Chem. 272:1038-1045(1997).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA   Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA   Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA   Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA   Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
RA   Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA   Sagripanti J.L.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU-355.
RA   Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA   Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RT   "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SULFATION OF TYR-26, AND N-GLYCOSYLATION.
RX   MEDLINE=20501139; PubMed=11046064;
RA   Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
RA   Chakravarty L., Kolattukudy P.E.;
RT   "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
RT   has tyrosine sulfation in a conserved extracellular N-terminal
RT   region.";
RL   J. Immunol. 165:5295-5303(2000).
CC   -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC       Transduces a signal by increasing the intracellular calcium ions
CC       level. Alternative coreceptor with CD4 for HIV-1 infection.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=A;
CC         IsoId=P41597-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=P41597-2; Sequence=VSP_001893;
CC   -!- PTM: N-glycosylated.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
```

```
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; U03882; AAA19119.1; -.
DR   EMBL; U03905; AAA19120.1; -.
DR   EMBL; D29984; BAA06253.1; -.
DR   EMBL; U80924; AAC51637.1; -.
DR   EMBL; U80924; AAC51636.1; -.
DR   EMBL; U95626; AAB57791.1; -.
DR   EMBL; U95626; AAB57792.1; -.
DR   EMBL; AF545480; AAN16400.1; -.
DR   PIR; I38450; I38450.
DR   PIR; JC2443; JC2443.
DR   PDB; 1KAD; Model; A=1-349.
DR   PDB; 1KP1; Model; A=1-349.
DR   Genew; HGNC:1603; CCR2.
DR   MIM; 601267; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0004950; F:chemokine receptor activity; TAS.
DR   GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.
DR   GO; GO:0006968; P:cellular defense response; TAS.
DR   GO; GO:0006935; P:chemotaxis; TAS.
DR   GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   GO; GO:0007259; P:JAK-STAT cascade; TAS.
DR   GO; GO:0007194; P:negative regulation of adenylate cyclase ac. . .; TAS.
DR   InterPro; IPR002237; CC_2_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   3D-structure; Alternative splicing; G-protein coupled receptor;
KW   Glycoprotein; Polymorphism; Sulfation; Transmembrane.
FT   DOMAIN        1     42       Extracellular (Potential).
FT   TRANSMEM     43     70       1 (Potential).
FT   DOMAIN       71     80       Cytoplasmic (Potential).
FT   TRANSMEM     81    100       2 (Potential).
FT   DOMAIN      101    114       Extracellular (Potential).
FT   TRANSMEM    115    136       3 (Potential).
FT   DOMAIN      137    153       Cytoplasmic (Potential).
FT   TRANSMEM    154    178       4 (Potential).
FT   DOMAIN      179    206       Extracellular (Potential).
FT   TRANSMEM    207    226       5 (Potential).
FT   DOMAIN      227    243       Cytoplasmic (Potential).
FT   TRANSMEM    244    268       6 (Potential).
FT   DOMAIN      269    285       Extracellular (Potential).
FT   TRANSMEM    286    309       7 (Potential).
FT   DOMAIN      310    374       Cytoplasmic (Potential).
FT   CARBOHYD     14     14       N-linked (GlcNAc. . .) (Potential).
FT   MOD_RES      26     26       Sulfotyrosine.
FT   DISULFID    113    190       By similarity.
```

```
FT   VARSPLIC    314     374       SLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGR
FT                                 GKGKSIGRAPEASLQDKEGA -> RYLSVFFRKHITKRFCK
FT                                 QCPVFYRETVDGVTSTNTPSTGEQEVSAGL (in
FT                                 isoform B).
FT                                 /FTId=VSP_001893.
FT   VARIANT      64      64       V -> I (in dbSNP:1799864).
FT                                 /FTId=VAR_014339.
FT   VARIANT     355     355       G -> E.
FT                                 /FTId=VAR_014340.
SQ   SEQUENCE   374 AA;  41914 MW;  F865E0D39E74CF0F CRC64;

  Query Match             100.0%;  Score 1970;  DB 1;  Length 374;
  Best Local Similarity   100.0%;  Pred. No. 1e-118;
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360

Qy        361 GRAPEASLQDKEGA 374
              ||||||||||||||
Db        361 GRAPEASLQDKEGA 374


RESULT 2
CKR2_MACMU
ID   CKR2_MACMU     STANDARD;      PRT;   360 AA.
AC   O18793;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
DE   (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
GN   Name=CCR2; Synonyms=CMKBR2;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
```

```
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21354176; PubMed=11461684; DOI=10.1089/088922201750290104;
RA   Margulies B.J., Hauer D.A., Clements J.E.;
RT   "Identification and comparison of eleven rhesus macaque chemokine
RT   receptors.";
RL   AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC   -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC       Transduces a signal by increasing the intracellular calcium ions
CC       level.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=B;
CC         IsoId=O18793-1; Sequence=Displayed;
CC       Name=A;
CC         IsoId=O18793-2; Sequence=Not described;
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF013958; AAD11572.1; -.
DR   InterPro; IPR002237; CC_2_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW   Sulfation; Transmembrane.
FT   DOMAIN        1     42       Extracellular (Potential).
FT   TRANSMEM     43     70       1 (Potential).
FT   DOMAIN       71     80       Cytoplasmic (Potential).
FT   TRANSMEM     81    100       2 (Potential).
FT   DOMAIN      101    114       Extracellular (Potential).
FT   TRANSMEM    115    136       3 (Potential).
FT   DOMAIN      137    153       Cytoplasmic (Potential).
FT   TRANSMEM    154    178       4 (Potential).
FT   DOMAIN      179    206       Extracellular (Potential).
FT   TRANSMEM    207    226       5 (Potential).
FT   DOMAIN      227    243       Cytoplasmic (Potential).
FT   TRANSMEM    244    268       6 (Potential).
FT   DOMAIN      269    285       Extracellular (Potential).
FT   TRANSMEM    286    309       7 (Potential).
FT   DOMAIN      310    360       Cytoplasmic (Potential).
FT   CARBOHYD     14     14       N-linked (GlcNAc. . .) (Potential).
FT   MOD_RES      26     26       Sulfotyrosine (By similarity).
FT   DISULFID    113    190       By similarity.
```

```
SQ   SEQUENCE   360 AA;  41139 MW;  4B2552BCE913FE9F CRC64;

  Query Match             82.0%;  Score 1614.5;  DB 1;  Length 360;
  Best Local Similarity   96.6%;  Pred. No. 6.1e-96;
  Matches  308;  Conservative    4;  Mismatches    4;  Indels    3;  Gaps    1;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLSTSRSRFIRNTNGSGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db         61 MLVVLILINCKKLKSLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 HIGYLGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ||:|||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CQEEDSVYICGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              |||:|||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        241 AVRLIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTRQLDQATQVTETLGMTHCCI 300

Qy        301 NPIIYAFVGEKFR---SLF 316
              |||||||||||||   |:|
Db        301 NPIIYAFVGEKFRRYLSMF 319


RESULT 3
CKR2_RAT
ID   CKR2_RAT       STANDARD;      PRT;   373 AA.
AC   O55193;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2).
GN   Name=Ccr2; Synonyms=Cmkbr2;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=98318173; PubMed=9655467; DOI=10.1016/S0165-5728(98)00005-8;
RA   Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA   deFiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT   "Chemokine receptor expression in cultured glia and rat experimental
RT   allergic encephalomyelitis.";
RL   J. Neuroimmunol. 86:1-12(1998).
CC   -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC       chemokines. Transduces a signal by increasing the intracellular
CC       calcium ions level (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
```

```
CC   -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
CC       macrophages.
CC   -!- INDUCTION: In animals in which experimental allergic
CC       encephalomyelitis (EAE) has been induced.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U77349; AAC03242.1; -.
DR   RGD; 620876; Ccr2.
DR   InterPro; IPR002237; CC_2_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane.
FT   DOMAIN        1     60       Extracellular (Potential).
FT   TRANSMEM     61     81       Potential.
FT   DOMAIN       82     91       Cytoplasmic (Potential).
FT   TRANSMEM     92    112       Potential.
FT   DOMAIN      113    128       Extracellular (Potential).
FT   TRANSMEM    129    149       Potential.
FT   DOMAIN      150    170       Cytoplasmic (Potential).
FT   TRANSMEM    171    191       Potential.
FT   DOMAIN      192    220       Extracellular (Potential).
FT   TRANSMEM    221    241       Potential.
FT   DOMAIN      242    256       Cytoplasmic (Potential).
FT   TRANSMEM    257    277       Potential.
FT   DOMAIN      278    301       Extracellular (Potential).
FT   TRANSMEM    302    322       Potential.
FT   DOMAIN      323    373       Cytoplasmic (Potential).
FT   DISULFID    126    203       By similarity.
SQ   SEQUENCE   373 AA;  42763 MW;  2E7BB012F5D6FD09 CRC64;

  Query Match             68.4%;  Score 1346.5;  DB 1;  Length 373;
  Best Local Similarity   76.9%;  Pred. No. 9.5e-79;
  Matches  257;  Conservative   25;  Mismatches   45;  Indels    7;  Gaps    3;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              :|||| | | |:  |  |  || :||| | ||||  |||||| :|||||||||||||||
Db         14 ILSTSHSLFPRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN 73

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              |||::|||:||||| :||||| |||||||||:||| ||| |||||||| |||||||||
Db         74 MLVIIILISCKKLKSMTDIYLFNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKLFTGLY 133

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              |||||||||||||||||||||||||||||||||||:|||:||:|||||:|||||||
Db        134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVITSVVTWVVAVFASLPGIIFTK 193
```

```
Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
              ::||  : ||||||  | || ||||||| |:||||:||||||||| || ||||||||||
Db        194 SEQEDDQHTCGPYFPTIWKNFQTIMRNILSLILPLLVMVICYSGILHTLFRCRNEKKRHR 253

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              |||:|| |||||||||||||||: | ||||| |:|||     |||| ||||||||||||:
Db        254 AVRLIFAIMIVYFLFWTPYNIVLFLTTFQEFLGMSNCVVDMHLDQAMQVTETLGMTHCCV 313

Qy        301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
              |||||||||||||   |:|   |||   |:  |:
Db        314 NPIIYAFVGEKFRRYLSIFFRKHIAKNLCKQCPV 347


RESULT 4
CKR2_MOUSE
ID   CKR2_MOUSE     STANDARD;      PRT;   373 AA.
AC   P51683; Q61172;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
DE   (JE/FIC receptor) (MCP-1 receptor).
GN   Name=Ccr2; Synonyms=Cmkbr2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96205938; PubMed=8631787; DOI=10.1074/jbc.271.13.7551;
RA   Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
RA   Charo I.F.;
RT   "Molecular cloning and functional expression of murine JE (monocyte
RT   chemoattractant protein 1) and murine macrophage inflammatory protein
RT   1alpha receptors: evidence for two closely linked C-C chemokine
RT   receptors on chromosome 9.";
RL   J. Biol. Chem. 271:7551-7558(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=96216064; PubMed=8662823; DOI=10.1074/jbc.271.20.11603;
RA   Kurihara T., Bravo R.;
RT   "Cloning and functional expression of mCCR2, a murine receptor for the
RT   C-C chemokines JE and FIC.";
RL   J. Biol. Chem. 271:11603-11606(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97026720; PubMed=8872898;
RX   DOI=10.1002/(SICI)1097-4547(19960815)45:4<382::AID-JNR7>3.3.CO;2-H;
RA   Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
RA   Post T.W., Gerard C., Dorf M.E.;
RT   "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
RT   transcriptase-polymerase chain reaction does not detect mRNA for the
RT   KC or new MCP-1 receptor.";
RL   J. Neurosci. Res. 45:382-391(1996).
CC   -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
```

```
CC       chemokines. Transduces a signal by increasing the intracellular
CC       calcium ions level.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC       but not in nonhematopoietic cell lines.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U47035; AAC52453.1; -.
DR   EMBL; U51717; AAC52557.1; -.
DR   EMBL; U56819; AAC52784.1; -.
DR   MGD; MGI:106185; Ccr2.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
DR   GO; GO:0019955; F:cytokine binding; IPI.
DR   GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.
DR   GO; GO:0030097; P:hemopoiesis; IMP.
DR   GO; GO:0006959; P:humoral immune response; IMP.
DR   GO; GO:0006954; P:inflammatory response; IMP.
DR   GO; GO:0019233; P:perception of pain; IMP.
DR   GO; GO:0030334; P:regulation of cell migration; IMP.
DR   InterPro; IPR002237; CC_2_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane.
FT   DOMAIN        1     55       Extracellular (Potential).
FT   TRANSMEM     56     83       1 (Potential).
FT   DOMAIN       84     93       Cytoplasmic (Potential).
FT   TRANSMEM     94    114       2 (Potential).
FT   DOMAIN      115    127       Extracellular (Potential).
FT   TRANSMEM    128    149       3 (Potential).
FT   DOMAIN      150    166       Cytoplasmic (Potential).
FT   TRANSMEM    167    191       4 (Potential).
FT   DOMAIN      192    219       Extracellular (Potential).
FT   TRANSMEM    220    239       5 (Potential).
FT   DOMAIN      240    256       Cytoplasmic (Potential).
FT   TRANSMEM    257    281       6 (Potential).
FT   DOMAIN      282    298       Extracellular (Potential).
FT   TRANSMEM    299    322       7 (Potential).
FT   DOMAIN      323    373       Cytoplasmic (Potential).
FT   DISULFID    126    203       By similarity.
FT   CONFLICT     39     39       Y -> H (in Ref. 1).
FT   CONFLICT    184    184       A -> G (in Ref. 1).
FT   CONFLICT    264    264       V -> G (in Ref. 1).
SQ   SEQUENCE   373 AA;  42782 MW;  FA012C10F4C9325A CRC64;

  Query Match             67.6%;  Score 1332.5;  DB 1;  Length 373;
```

```
  Best Local Similarity   76.3%;  Pred. No. 7.5e-78;
  Matches  255;  Conservative   26;  Mismatches   46;  Indels    7;  Gaps    3;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              :|||| | | |:  |  |  || :||| | ||||  |||||| :|||||||||||||||
Db         14 ILSTSHSLFTRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN 73

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              |||::||| ||||| :||||||||||||||||:||| ||| |||||||| |||:|||||
Db         74 MLVIIILIGCKKLKSMTDIYLLNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKVFTGLY 133

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              |||||||||||||||||||||||||||||||||||:|||:||:||||||:|||||||
Db        134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVITSVVTWVVAVFASLPGIIFTK 193

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
               :::|  | ||||| : | || ||||||| |:||||:||||||||| || ||||||||||
Db        194 SKQDDHHYTCGPYFTQLWKNFQTIMRNILSLILPLLVMVICYSGILHTLFRCRNEKKRHR 253

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              |||:|| |||||||||||||||: | ||||  |:|||     |||| ||||||||||||
Db        254 AVRLIFAIMIVYFLFWTPYNIVLFLTTFQESLGMSNCVIDKHLDQAMQVTETLGMTHCCI 313

Qy        301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
              ||:||||||||||   |:|   |||   |:  |:
Db        314 NPVIYAFVGEKFRRYLSIFFRKHIAKRLCKQCPV 347


RESULT 5
Q6YT42
ID   Q6YT42      PRELIMINARY;      PRT;   373 AA.
AC   Q6YT42;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Chemokine (C-C motif) receptor 2 (Chemokine C-C motif receptor
DE   2).
GN   Name=CCR2;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
RA   Uenishi H.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP006185; BAD08648.1; -.
DR   EMBL; AP006435; BAD08655.1; -.
```

```
DR   EMBL; AB119271; BAD12134.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR002237; CC_2_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR01107; CHEMOKINER2.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   373 AA;  42299 MW;  FA8E55CA527A34E0 CRC64;

  Query Match             67.4%;  Score 1327.5;  DB 2;  Length 373;
  Best Local Similarity   76.0%;  Pred. No. 1.6e-77;
  Matches  254;  Conservative   29;  Mismatches   44;  Indels    7;  Gaps    3;

Qy          1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
              :| || |    |   : || || :||||  || |  | || | ||||||||||||||||
Db         14 VLPTSHSLLTMNIKGNDEEPTTSYDYDYSEPCQKTSVGQIEALLLPPLYSLVFIFGFVGN 73

Qy         61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
              :|||||||||||||| :|||||||||||||||| |:| ||| ||::|||||| ||| |||||
Db         74 LLVVLILINCKKLKSMTDIYLLNLAISDLLFLFTIPFWAHYAADQWVFGNIMCKFFTGLY 133

Qy        121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
              |||||||||||||||||||||||||||||||||||||||||| :||:||:|||:||||| :
Db        134 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSGVTWVVAIFASLPGIIFIR 193

Qy        181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
               |:| | | | ||||  | |||||||:||||||||:||:||||||||||||||||:|:
Db        194 SQEEHSGYACAPYFPLAWKNFHTIMRSILGLVLPLLVMVVCYSGILKTLLRCRNEKKKHK 253

Qy        241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
              |||:|| |||||||| |||||:||:||| |||||||:::|||||| |||||||:|||||
Db        254 AVRLIFVIMIVYFLFWAPYNIVLLLSTFQVFFGLSNCKNSSQLDQAMQVTETLGLTHCCI 313

Qy        301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
              |||||||||||||   |:|   |||   |:  |:
Db        314 NPIIYAFVGEKFRRYLSVFFRKHIAKHLCKQCPV 347


RESULT 6
Q95NC2
ID   Q95NC2      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   C-C chemokine receptor 5.
GN   Name=CCR5;
OS   Callicebus moloch (Dusky titi).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Callicebinae;
OC   Callicebus.
OX   NCBI_TaxID=9523;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AF177887; AAK43370.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR002240; CC_5_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR01110; CHEMOKINER5.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   352 AA;  40495 MW;  7FB307513ACF9B9B CRC64;

  Query Match             63.6%;  Score 1252;  DB 2;  Length 352;
  Best Local Similarity   76.1%;  Pred. No. 1e-72;
  Matches  239;  Conservative   26;  Mismatches   37;  Indels   12;  Gaps    3;

Qy         18 EEVTTFFDYDYGA--PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKC 75
              |  :  :| ||||  || | ||||:||||||||||:||:||||||||||||||||:||
Db          4 EVSSPIYDIDYGASEPCQKIDVKQMGAQLLPPLYSMVFLFGFVGNMLVVLILINCKRLKS 63

Qy         76 LTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLT 135
              :|||||||||||| || |:| ||| || :| ||| ||:  |||| ||:| |||||||||
Db         64 MTDIYLLNLAISDLFFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLT 123

Qy        136 IDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP 195
              |||||||||||||||||||||||||||||:||||||:||||||: |||   | | |:||
Db        124 IDRYLAIVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGYHYTCSPHFP 183

Qy        196 RG----WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIV 251
               |    | |  |:   |||||||||:||||||||||||||||||||||||:|||||||
Db        184 FGQYRFWKNLETLKMVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIV 243

Qy        252 YFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEK 311
              ||||| |||||:||||:||||||:|| |:::|||| |||||||||||:||||||||||
Db        244 YFLFWAPYNIVLLLNTYQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEK 303

Qy        312 FRSLF------HIA 319
              ||:        |||
Db        304 FRNYLLVFFQKHIA 317
```

```
RESULT 7
Q68G28
ID   Q68G28      PRELIMINARY;      PRT;   354 AA.
AC   Q68G28;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Chemokine (C-C) receptor 5.
GN   Name=Cmkbr5;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Director MGC Project;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC078756; AAH78756.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR002240; CC_5_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR01110; CHEMOKINER5.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
```

```
KW   Receptor.
SQ   SEQUENCE   354 AA;  41081 MW;  4CCB9A9C4EEE985C CRC64;

  Query Match             63.3%;  Score 1247;  DB 2;  Length 354;
  Best Local Similarity   75.6%;  Pred. No. 2.2e-72;
  Matches  233;  Conservative   29;  Mismatches   40;  Indels    6;  Gaps    2;

Qy         17 GEEVTTFFDYDY--GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLK 74
              |   |  :| ||   ||| ||:|||| ||||||||||||||||||||:| ||||:|||||
Db          5 GSIPTYIYDIDYSMSAPCQKFNVKQIAAQLLPPLYSLVFIFGFVGNMMVFLILISCKKLK 64

Qy         75 CLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILL 134
              :|||||| ||||||||||:||| ||| |||||||| |||||||:||||||||||||||
Db         65 SMTDIYLFNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKLFTGIYHIGYFGGIFFIILL 124

Qy        135 TIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYF 194
              |||||||||||||||:|||| |||:|||:||:|||| |:| ||| : ||| | | | |:|
Db        125 TIDRYLAIVHAVFAIKARTVNFGVITSVVTWVVAVFVSLPEIIFMRSQKEGSHYTCSPHF 184

Qy        195 P----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMI 250
              |    | | :| |:   || |:||||:||||||||| || ||||||||||||:|| |||
Db        185 PRIQYRFWKHFQTLKMVILSLILPLLVMVICYSGILNTLFRCRNEKKRHRAVRLIFAIMI 244

Qy        251 VYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGE 310
              |||||||||||:|| ||||:|||:|| |:::|||| ||||||||||:||:|||||||
Db        245 VYFLFWTPYNIVLLLTTFQEYFGLNNCSSSNRLDQAMQVTETLGMTHCCLNPVIYAFVGE 304

Qy        311 KFRSLFHI 318
              |||:   :
Db        305 KFRNYLSV 312


RESULT 8
Q9TQT3
ID   Q9TQT3      PRELIMINARY;      PRT;   339 AA.
AC   Q9TQT3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   C-C chemokine receptor 5 (Fragment).
GN   Name=CCR5;
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22942991; PubMed=14581567;
RX   DOI=10.1128/JVI.77.22.12310-12318.2003;
RA   Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R.,
RA   Kunstman J., Stanton J., Agy M., Shibata R., Yoder A.D., Pillai S.,
RA   Doms R.W., Marx P., Wolinsky S.M.;
RT   "Structure and function of CC-chemokine receptor 5 homologues derived
RT   from representative primate species and subspecies of the taxonomic
RT   suborders Prosimii and Anthropoidea.";
RL   J. Virol. 77:12310-12318(2003).
RN   [2]
```

```
RP   SEQUENCE FROM N.A.
RA   Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA   Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AF162021; AAD47776.1; -.
DR   EMBL; AF161934; AAD47691.1; -.
DR   EMBL; AF161935; AAD47692.1; -.
DR   EMBL; AF161936; AAD47693.1; -.
DR   EMBL; AF161937; AAD47694.1; -.
DR   EMBL; AF161938; AAD47695.1; -.
DR   EMBL; AF161939; AAD47696.1; -.
DR   EMBL; AF161940; AAD47697.1; -.
DR   EMBL; AF161944; AAD47700.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR002240; CC_5_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR01110; CHEMOKINER5.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
FT   NON_TER       1      1
FT   NON_TER     339    339
SQ   SEQUENCE   339 AA;  39055 MW;  C1313952E71B50C7 CRC64;

  Query Match             63.1%;  Score 1244;  DB 2;  Length 339;
  Best Local Similarity   76.6%;  Pred. No. 3.3e-72;
  Matches  236;  Conservative   27;  Mismatches   33;  Indels   12;  Gaps    3;

Qy         24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
              :| |||   || | ||||:|| |||||||:||:||||||||||||||||:|| :|||||
Db          3 YDIDYGPSEPCRKIDVKQMGAHLLPPLYSMVFLFGFVGNMLVVLILINCKRLKSMTDIYL 62

Qy         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
              ||||||||:|| |:| ||| || :| ||| ||:  |||| ||:| ||||||||||||||
Db         63 LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 122

Qy        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
              |||||||||||||||||||||||:||||||:||||||: |||   | | |:||    :
Db        123 IVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGYHYTCSPHFPFSQYQF 182

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              | || |:  ·|||||||||:||||||||||||||||||||||||:||||||||||||
Db        183 WKNFETLKMVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 242

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
```

```
              |||||:||||:||||||:|| |:::|||| ||||||||||||:||||||||||||:
Db        243 PYNIVLLLNTYQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLA 302

Qy        317 -----HIA 319
                  |||
Db        303 VFFQKHIA 310
```

```
RESULT 9
Q9TUV8
ID   Q9TUV8      PRELIMINARY;      PRT;   339 AA.
AC   Q9TUV8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   C-C chemokine receptor 5 (Fragment).
GN   Name=CCR5;
OS   Saguinus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX   NCBI_TaxID=100754;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22942991; PubMed=14581567;
RX   DOI=10.1128/JVI.77.22.12310-12318.2003;
RA   Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R.,
RA   Kunstman J., Stanton J., Agy M., Shibata R., Yoder A.D., Pillai S.,
RA   Doms R.W., Marx P., Wolinsky S.M.;
RT   "Structure and function of CC-chemokine receptor 5 homologues derived
RT   from representative primate species and subspecies of the taxonomic
RT   suborders Prosimii and Anthropoidea.";
RL   J. Virol. 77:12310-12318(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA   Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AF161929; AAD47686.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR002240; CC_5_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR01110; CHEMOKINER5.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
```

```
FT   NON_TER       1      1
FT   NON_TER     339    339
SQ   SEQUENCE   339 AA;  39164 MW;  6A67CF5D22C70C49 CRC64;

  Query Match             63.1%;  Score 1244;  DB 2;  Length 339;
  Best Local Similarity   77.3%;  Pred. No. 3.3e-72;
  Matches  238;  Conservative   24;  Mismatches   34;  Indels   12;  Gaps    3;

Qy         24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
              :| |||   || | ||||:|| |||||||:||:||||||||||||||||: | :|||||
Db          3 YDIDYGPSEPCRKIDVKQMGAHLLPPLYSMVFLFGFVGNMLVVLILINCKRPKSMTDIYL 62

Qy         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
              ||||||||:|| |:| ||| || :| ||| ||:  |||| ||:| ||||||||||||||
Db         63 LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 122

Qy        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---- 197
              |||||||||||||||||||||||||||||:||||||: |||   | | |::| |
Db        123 IVHAVFALKARTVTFGVVTSVITWLVAVFASLPGIIFTRSQKEGYHYTCSPHYPFGQYQF 182

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              | || |:   |||||||||||||||||||||||||||||||||||:||||||||||||
Db        183 WKNFETLKMVILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 242

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
              |||||:||||:||||||:|| |:::|||| |||||||||||||||||||||||||||:
Db        243 PYNIVLLLNTYQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLV 302

Qy        317 -----HIA 319
                    |||
Db        303 VFFQKHIA 310


RESULT 10
Q6WN98
ID   Q6WN98      PRELIMINARY;      PRT;   352 AA.
AC   Q6WN98;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   CC chemokine receptor 5.
GN   Name=ccr5;
OS   Callithrix humeralifera (Tassel-eared marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX   NCBI_TaxID=52232;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
RA   Seuanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;
RT   "CCR5 chemokine receptor gene evolution in new world monkeys
RT   (Platyrrhini, Primates): implication on resistance to lentiviruses.";
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AY278745; AAQ20013.1; -.
DR   EMBL; AY278744; AAQ20012.1; -.
```

```
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR002240; CC_5_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR01110; CHEMOKINER5.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   352 AA;  40522 MW;  FF0D0A852E553AF5 CRC64;

  Query Match             63.1%;  Score 1244;  DB 2;  Length 352;
  Best Local Similarity   76.6%;  Pred. No. 3.4e-72;
  Matches  236;  Conservative   27;  Mismatches   33;  Indels   12;  Gaps    3;

Qy         24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
              :| |||   || | ||||:|| |||||||:||:||||||||||||||||:|| :|||||
Db         10 YDIDYGPSEPCRKIDVKQMGAHLLPPLYSMVFLFGFVGNMLVVLILINCKRLKSMTDIYL 69

Qy         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
              ||||||||:|| |:| ||| || :| ||| ||:  |||| ||:| ||||||||||||||
Db         70 LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 129

Qy        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
              ||||||||||||||||||||||:||||||:||||||: |||   | | |:||    :
Db        130 IVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGYHYTCSPHFPFSQYQF 189

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              | || |:   |||||||||:||||||||||||||||||||||||:||||||||||
Db        190 WKNFETLKMVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
              |||||:||||:||||||:|| |:::|||| ||||||||||:||||||||||||:
Db        250 PYNIVLLLNTYQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLK 309

Qy        317 -----HIA 319
                   |||
Db        310 VFFQKHIA 317


RESULT 11
Q9MZA0
ID   Q9MZA0      PRELIMINARY;      PRT;   352 AA.
AC   Q9MZA0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   CC chemokine receptor 5 (Chemokine receptor CCR5).
GN   Name=CCR5; Synonyms=ccr5;
```

OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20317091; PubMed=10747879; DOI=10.1074/jbc.M000169200;
RA Mummidi S., Bamshad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,
RA Begum K., Galvis M.C., Kostecki V., Valente A.J., Murthy K.K.,
RA Haro L., Dolan M.J., Allan J.S., Ahuja S.K.;
RT "Evolution of human and non-human primate CC chemokine receptor 5 gene
RT and mRNA. Potential roles for haplotype and mRNA diversity,
RT differential haplotype-specific transcriptional activity, and altered
RT transcription factor binding to polymorphic nucleotides in the
RT pathogenesis of HIV-1 and simian immunodeficiency virus.";
RL J. Biol. Chem. 275:18946-18961(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22174698; PubMed=12186836;
RA LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT "Blockade of HIV-1 infection of New World monkey cells occurs
RT primarily at the stage of virus entry.";
RL J. Exp. Med. 196:431-445(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
RA Seuanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF252554; AAF87984.1; -.
DR EMBL; AF452614; AAN14530.1; -.
DR EMBL; AY278743; AAQ20011.1; -.
DR EMBL; AF177878; AAK43361.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR002240; CC_5_receptor.
DR InterPro; IPR000355; Chmkine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 352 AA; 40465 MW; FF0D0A8D06F7B8F5 CRC64;

```
  Query Match             63.1%;  Score 1244;  DB 2;  Length 352;
  Best Local Similarity   76.6%;  Pred. No. 3.4e-72;
  Matches  236;  Conservative   27;  Mismatches   33;  Indels   12;  Gaps    3;

Qy         24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
              :| |||   || | ||||:|| |||||||:||:||||||||||||||||:|| :|||||
Db         10 YDIDYGPSEPCRKIDVKQMGAHLLPPLYSMVFLFGFVGNMLVVLILINCKRLKSMTDIYL 69

Qy         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
              ||||||||:|| |:| ||| || :| ||| ||:  |||| ||:| ||||||||||||||
Db         70 LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 129

Qy        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
              |||||||||||||||||||||||:||||||:||||||: |||   | | |:||    :
Db        130 IVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGYHYTCSPHFPFSQYQF 189

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              | || |:   |||||||||:||||||||||||||||||||||||:||||||||||||
Db        190 WKNFETLKMVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
              |||||:||||:||||||:|| |:::|||| ||||||||||||:||||||||||||||:
Db        250 PYNIVLLLNTYQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLA 309

Qy        317 -----HIA 319
                  |||
Db        310 VFFQKHIA 317


RESULT 12
CKR5_MOUSE
ID   CKR5_MOUSE     STANDARD;      PRT;   354 AA.
AC   P51682; O35313; O35891; P97308; P97405; Q61867;
DT   01-OCT-1996 (Rel. 34, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1
DE   alpha receptor).
GN   Name=Ccr5; Synonyms=Cmkbr5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ; TISSUE=Spleen;
RX   MEDLINE=96205938; PubMed=8631787; DOI=10.1074/jbc.271.13.7551;
RA   Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
RA   Charo I.F.;
RT   "Molecular cloning and functional expression of murine JE (monocyte
RT   chemoattractant protein 1) and murine macrophage inflammatory protein
RT   1alpha receptors: evidence for two closely linked C-C chemokine
RT   receptors on chromosome 9.";
RL   J. Biol. Chem. 271:7551-7558(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
```

```
RX   MEDLINE=96278910; PubMed=8662890; DOI=10.1074/jbc.271.24.14445;
RA   Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT   "Cloning and characterization of a novel murine macrophage
RT   inflammatory protein-1 alpha receptor.";
RL   J. Biol. Chem. 271:14445-14451(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Ola;
RA   Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
RX   MEDLINE=98001387; PubMed=9343222;
RA   Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT   "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT   implicate specific amino acids in infections by simian and human
RT   immunodeficiency viruses.";
RL   J. Virol. 71:8642-8656(1997).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129;
RX   MEDLINE=97404635; PubMed=9261347;
RA   Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
RA   Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
RT   "Two distinct CCR5 domains can mediate coreceptor usage by human
RT   immunodeficiency virus type 1.";
RL   J. Virol. 71:6305-6314(1997).
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Guo B., Kuno K., Harada A., Matsushima K.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC       MIP-1-beta and RANTES and subsequently transduces a signal by
CC       increasing the intracellular calcium ions level.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC       but not in nonhematopoietic cell lines.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U47036; AAC52454.1; -.
DR   EMBL; X94151; CAA63867.1; -.
DR   EMBL; U68565; AAB37273.1; -.
DR   EMBL; U83327; AAC53386.1; -.
DR   EMBL; AF022990; AAC53389.1; -.
DR   EMBL; AF019772; AAB71183.1; -.
DR   EMBL; D83648; BAA12024.1; -.
DR   MGD; MGI:107182; Ccr5.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
```

```
DR   GO; GO:0006952; P:defense response; IMP.
DR   InterPro; IPR002240; CC_5_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.
FT   DOMAIN        1     32       Extracellular (Potential).
FT   TRANSMEM     33     60       1 (Potential).
FT   DOMAIN       61     70       Cytoplasmic (Potential).
FT   TRANSMEM     71     91       2 (Potential).
FT   DOMAIN       92    104       Extracellular (Potential).
FT   TRANSMEM    105    126       3 (Potential).
FT   DOMAIN      127    143       Cytoplasmic (Potential).
FT   TRANSMEM    144    168       4 (Potential).
FT   DOMAIN      169    200       Extracellular (Potential).
FT   TRANSMEM    201    220       5 (Potential).
FT   DOMAIN      221    237       Cytoplasmic (Potential).
FT   TRANSMEM    238    262       6 (Potential).
FT   DOMAIN      263    279       Extracellular (Potential).
FT   TRANSMEM    280    303       7 (Potential).
FT   DOMAIN      304    354       Cytoplasmic (Potential).
FT   DISULFID    103    180       By similarity.
FT   CARBOHYD    270    270       N-linked (GlcNAc. . .) (Potential).
FT   VARIANT      11     11       I -> S.
FT   VARIANT      62     62       K -> R.
FT   VARIANT      66     66       V -> M.
FT   VARIANT      97     97       I -> V.
FT   VARIANT     109    109       V -> L.
FT   VARIANT     156    156       V -> A.
FT   VARIANT     160    160       F -> S.
FT   VARIANT     185    185       P -> L.
FT   VARIANT     213    213       I -> V.
FT   VARIANT     318    318       I -> M.
FT   VARIANT     337    337       V -> A.
FT   CONFLICT      3      3       F -> L (in Ref. 2).
FT   CONFLICT     80     80       L -> F (in Ref. 2).
FT   CONFLICT    145    145       N -> I (in Ref. 5).
FT   CONFLICT    190    190       H -> Y (in Ref. 3).
FT   CONFLICT    208    208       P -> S (in Ref. 1).
SQ   SEQUENCE   354 AA;  40863 MW;  B4A6B942E88F9CF0 CRC64;

  Query Match             63.1%;  Score 1244;  DB 1;  Length 354;
  Best Local Similarity   75.3%;  Pred. No. 3.4e-72;
  Matches  232;  Conservative   29;  Mismatches   41;  Indels    6;  Gaps    2;

Qy         17 GEEVTTFFDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLK 74
              |   |  :| |||  ||| | :|||| ||||||||||||||||||:| ||||:|||||
Db          5 GSVPTYIYDIDYGMSAPCQKINVKQIAAQLLPPLYSLVFIFGFVGNMMVFLILISCKKLK 64

Qy         75 CLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILL 134
              :|||||||||||||||:||| ||| |||||:||| |||:|||:|||||||||||||||
Db         65 SVTDIYLLNLAISDLLFLLTLPFWAHYAANEWIFGNIMCKVFTGVYHIGYFGGIFFIILL 124

Qy        135 TIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYF 194
```

```
                ||||||||||||||||| ||| |||:|||:||:||||||:| ||||: |||   | | |:|
Db        125 TIDRYLAIVHAVFALKVRTVNFGVITSVVTWVVAVFASLPEIIFTRSQKEGFHYTCSPHF 184

Qy        195 PRG----WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMI 250
                |      | :| |:   || |:||||:|:||||||| || ||||||||||||:|| |||
Db        185 PHTQYHFWKSFQTLKMVILSLILPLLVMIICYSGILHTLFRCRNEKKRHRAVRLIFAIMI 244

Qy        251 VYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGE 310
                ||||||||||||:|| ||||||||:|| |:::|||| | ||||||||||:||:|||||||
Db        245 VYFLFWTPYNIVLLLTTFQEFFGLNNCSSSNRLDQAMQATETLGMTHCCLNPVIYAFVGE 304

Qy        311 KFRSLFHI 318
                ||||   :
Db        305 KFRSYLSV 312
```

```
RESULT 13
Q9TQV5
ID   Q9TQV5      PRELIMINARY;      PRT;   339 AA.
AC   Q9TQV5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   C-C chemokine receptor 5 (Fragment).
GN   Name=CCR5;
OS   Saguinus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX   NCBI_TaxID=100754;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22942991; PubMed=14581567;
RX   DOI=10.1128/JVI.77.22.12310-12318.2003;
RA   Kunstman K.J., Puffer B., Korber B.T., Kuiken C., Smith U.R.,
RA   Kunstman J., Stanton J., Agy M., Shibata R., Yoder A.D., Pillai S.,
RA   Doms R.W., Marx P., Wolinsky S.M.;
RT   "Structure and function of CC-chemokine receptor 5 homologues derived
RT   from representative primate species and subspecies of the taxonomic
RT   suborders Prosimii and Anthropoidea.";
RL   J. Virol. 77:12310-12318(2003).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA   Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinksy S.;
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AF161931; AAD47688.1; -.
DR   EMBL; AF161925; AAD47682.1; -.
DR   EMBL; AF161926; AAD47683.1; -.
DR   EMBL; AF161923; AAD47680.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000923; BlueCu_1.
```

```
DR   InterPro; IPR002240; CC_5_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR01110; CHEMOKINER5.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
FT   NON_TER       1      1
FT   NON_TER     339    339
SQ   SEQUENCE   339 AA;  39081 MW;  6B79D05D22C70032 CRC64;

  Query Match             63.1%;  Score 1243;  DB 2;  Length 339;
  Best Local Similarity   76.9%;  Pred. No. 3.8e-72;
  Matches  237;  Conservative   25;  Mismatches   34;  Indels   12;  Gaps    3;

Qy         24 FDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
              :| |||   || | ||||:|| |||||||:||:||||||||||||||||: | :|||||
Db          3 YDIDYGPSEPCRKIDVKQMGAHLLPPLYSMVFLFGFVGNMLVVLILINCKRPKSMTDIYL 62

Qy         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
              ||||||||:|| |:| ||| || :| ||| ||:  |||| ||:| |||||||||||||||
Db         63 LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 122

Qy        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---- 197
              |||||||||||||||||||||||||||||:||||||: |||   | | |::| |
Db        123 IVHAVFALKARTVTFGVVTSVITWLVAVFASLPGIIFTRSQKEGYHYTCSPHYPFGQYQF 182

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              | || |:   |||||||||||||||||||||||||||||||||||:||||||||||||
Db        183 WKNFETLKMVILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 242

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
              |||||:||||:||||||:|| |:::|||| ||||||||||:||||||||||||||:
Db        243 PYNIVLLLNTYQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLV 302

Qy        317 -----HIA 319
                    |||
Db        303 VFFQKHIA 310


RESULT 14
Q95NC4
ID   Q95NC4      PRELIMINARY;      PRT;   352 AA.
AC   Q95NC4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   C-C chemokine receptor 5.
GN   Name=CCR5;
OS   Ateles geoffroyi (Black-handed spider monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Ateles.
OX   NCBI_TaxID=9509;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Ryder O.A., Zhang Y.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AF177885; AAK43368.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR002240; CC_5_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR01110; CHEMOKINER5.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   352 AA;  40440 MW;  F0A686CB4FE3964B CRC64;

  Query Match             63.1%;  Score 1243;  DB 2;  Length 352;
  Best Local Similarity   76.6%;  Pred. No. 4e-72;
  Matches  236;  Conservative   27;  Mismatches   33;  Indels   12;  Gaps    3;

Qy         24 FDYDYGA--PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
              :| ||||  || | ||||:|| |||||||:||:||||||||||||:|||: | :|||||
Db         10 YDIDYGASEPCRKTDVKQMGAHLLPPLYSMVFLFGFVGNMLVVLILVNCKRPKSMTDIYL 69

Qy         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
              |||||||||| |:| ||| || :| ||| ||:  |||| ||:| ||||||||||||||
Db         70 LNLAISDLLFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 129

Qy        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---- 197
              ||||||||||||||||:||||||:||||||:||||||: |||   | | |:|| |
Db        130 IVHAVFALKARTVTFGVMTSVITWVVAVFASLPGIIFTRSQKEGYHYTCSPHFPFGQYQF 189

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              | || |:   |||||||||:||||||||||||||||||||||||:||||||||||
Db        190 WKNFETLKMVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
              |||||:||||:||||||:|| |:::|||| ||||||||||:||||||||||||:
Db        250 PYNIVLLLNTYQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLL 309

Qy        317 -----HIA 319
                   |||
Db        310 VFFQKHIA 317


RESULT 15
Q6WN93
```

```
ID   Q6WN93      PRELIMINARY;      PRT;   352 AA.
AC   Q6WN93;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   CC chemokine receptor 5.
GN   Name=ccr5;
OS   Leontopithecus chrysopygus (Gold-and-black lion tamarin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC   Leontopithecus.
OX   NCBI_TaxID=58710;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Soares E.A.J.M., Schrago C.G., Ribeiro I.P., Pissinatti A.,
RA   Seuanez H.N., Russo C.A.M., Tanuri A., Soares M.A.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AY278750; AAQ20018.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000923; BlueCu_1.
DR   InterPro; IPR002240; CC_5_receptor.
DR   InterPro; IPR000355; Chmkine_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR01110; CHEMOKINER5.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   352 AA;  40437 MW;  5EC1884238503783 CRC64;

  Query Match             63.0%;  Score 1241;  DB 2;  Length 352;
  Best Local Similarity   76.3%;  Pred. No. 5.3e-72;
  Matches  235;  Conservative   27;  Mismatches   34;  Indels   12;  Gaps    3;

Qy         24 FDYDYGA--PCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
              :| ||||  || | ||||:|| |||||||:||:||||||||||:|||||: | :|||||
Db         10 YDIDYGASEPCRKIDVKQMGAHLLPPLYSMVFLFGFVGNMLVVLVLINCKRPKSMTDIYL 69

Qy         82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
              ||||||||:|| |:| ||| || :| ||| ||:  |||| ||:| |||||||||||||||
Db         70 LNLAISDLIFLFTVPFWAHYAAGQWDFGNTMCQFLTGLYFIGFFSGIFFIILLTIDRYLA 129

Qy        142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFPRG---- 197
              |||||||||||||||||||||||:||||||:||||||: |||   | | |:|| |
Db        130 IVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGYHYTCSPHFPFGQYQF 189

Qy        198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
              | ||  :   |||||||||:||||||||||||||||||||||||:||||||||||||
```

```
Db        190 WKNFEALKMVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA 249

Qy        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
              |||||:||||:||||||:|| |:::|||| ||||||||||||:||||||||||||||:
Db        250 PYNIVLLLNTYQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRNYLV 309

Qy        317 -----HIA 319
                  |||
Db        310 VFFRKHIA 317
```

Search completed: March 31, 2005, 14:06:57
Job time : 183 secs